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Multilevel Modelling of Event History Data: Comparing Methods Appropriate for Large Datasets

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Abstract

When analysing medical or public health datasets, it may often be of interest to measure the time until a particular pre-defined event occurs, such as death from some disease. As it is known that the health status of individuals living within the same area tends to be more similar than for individuals from different areas, event times of individuals from the same area may be correlated. As a result, multilevel models must be used to account for the clustering of individuals within the same geographical location. When the outcome is time until some event, multilevel event history models must be used.

Although software does exist for fitting multilevel event history models, such as MLwiN, computational requirements mean that the use of these models is limited for large datasets. For example, to fit the proportional hazards model (PHM), the most commonly used event history model for modelling the effect of risk factors on event times, in MLwiN a Poisson model is fitted to a person-period dataset. The person-period dataset is created by rearranging the original dataset so that each individual has a line of data corresponding to every risk set they survive until either censoring or the event of interest occurs. When time is treated as a continuous variable so that each risk set corresponds to a distinct event time, as is the case for the PHM, the size of the person-period dataset can be very large. This presents a problem for those working in public health as datasets used for measuring and monitoring public health are typically large. Furthermore, individuals may be followed-up for a long period of time and this can also contribute to a large person-period dataset. A further complication is that interest may be in modelling a rare event, resulting in a high proportion of censored observations. This can also be problematic when estimating multilevel event history models.

Since multilevel event history models are important in public health, the aim of this thesis is to develop these models so they can be fitted to large datasets considering, in particular, datasets with long periods of follow-up and rare events. Two datasets are used throughout the thesis to investigate three possible alternatives to fitting the multilevel proportional hazards model in MLwiN in order to overcome the problems discussed. The first is a moderately-

sized Scottish dataset, which will be the main focus of the thesis, and is used as a 'training dataset' to explore the limitations of existing software packages for fitting multilevel event history models and also for investigating alternative methods. The second dataset, from Sweden, is used to test the effectiveness of each alternative method when fitted to a much larger dataset. The adequacy of the alternative methods are assessed on the following criteria: how effective they are at reducing the size of the person-period dataset, how similar parameter estimates obtained from using methods are compared to the PHM and how easy they are to implement.

The first alternative method involves defining discrete-time risk sets and then estimating discrete-time hazard models via multilevel logistic regression models fitted to a person-period dataset. The second alternative method involves aggregating the data of individuals within the same higher-level units who have the same values for the covariates in a particular model. Aggregating the data like this means that one line of data is used to represent all such individuals since these individuals are at risk of experiencing the event of interest at the same time. This method is termed 'grouping according to covariates'. Both continuous-time and discrete-time event history models can be fitted to the aggregated person-period dataset. The 'grouping according to covariates' method and the first method, which involves defining discrete-time risk sets, are both implemented in MLwiN and pseudo-likelihood methods of estimation are used. The third and final method to be considered, however, involves fitting Bayesian event history (frailty) models and using Markov chain Monte Carlo (MCMC) methods of estimation. These models are fitted in WinBUGS, a software package specially designed to make practical MCMC methods available to applied statisticians. In WinBUGS, an additive frailty model is adopted and a Weibull distribution is assumed for the survivor function.

Methodological findings were that the discrete-time method led to a successful reduction in the continuous-time person-period dataset; however, it was necessary to experiment with the length of time intervals in order to have the widest interval without influencing parameter estimates. The grouping according to covariates method worked best when there were, on average, a larger number of individuals per higher-level unit, there were few risk factors in the model and little or none of the risk factors were continuous. The Bayesian

method could be favourable as no data expansion is required to fit the Weibull model in WinBUGS and time is treated as a continuous variable. However, models took a much longer time to run using MCMC methods of estimation as opposed to likelihood methods. This thesis showed that it was possible to use a re-parameterised version of the Weibull model, as well as a variance expansion technique, to overcome slow convergence by reducing correlation in the Markov chains. This may be a more efficient way to reduce computing time than running further iterations.

Table of Contents

Abstract	2
Acknowledgements	11
Author's Declaration	12
1 Introduction	13
1.1 The Use of Event History Models in Public Health	13
1.2 Introduction to Multilevel Modelling	14
1.3 Objectives	16
1.4 Computing Hardware	16
1.5 Overview of Thesis	17
2 Data Description	19
2.1 Introduction	19
2.2 The Moderately-Sized Scottish Dataset	19
2.3 The Larger Swedish Dataset	22
3 Mental Health and Psychiatric Admissions in Scotland	24
3.1 Introduction to Mental Health in Scotland	24
3.2 Recording and Detecting Mental Disorder in Scotland	26
3.2.1 The 12-item General Health Questionnaire (GHQ-12)	27
3.3 Risk Factors for Psychiatric Admission	31
3.3.1 Demographic Predictors	31
3.3.2 Socioeconomic Predictors	34
3.3.3 Lifestyle Predictors	37
3.4 Area Variations in Mental Illness	39
3.5 Objectives using Scottish Health Survey Data	41
4 Psychiatric Admissions in Scotland: Some Exploratory Analyses	43
4.1 Descriptive Statistics	43
4.1.1 Psychiatric Admissions in the Scottish Health Survey	43
4.1.2 Distribution of GHQ-12 Score in the Scottish Health Survey	45
4.1.3 Missing Data in the Scottish Health Survey	47
4.2 Applying Multilevel Modelling to Logistic Regression	48
4.3 Results from Multilevel Logistic Regression	51
4.4 Chapter Summary	55
5 Multilevel Event History Modelling: A Review	56
5.1 Introduction	56
5.2 Single-Level Survival Modelling	56
5.2.1 Introduction to Survival Modelling	56
5.2.2 Proportional Hazards Model	59
5.2.3 Accelerated Lifetime Model	61
5.3 Multilevel Survival Modelling	62
5.3.1 Extending the Single-Level Model	62
5.3.2 Software for Fitting Multilevel Models	63
5.3.3 Fitting a Multilevel Proportional Hazards Model in MLwiN	64
5.3.4 Fitting a Multilevel Accelerated Lifetime Model in MLwiN	73
5.3.5 Estimation of Parameters in MLwiN	74
5.4 Multilevel Survival Modelling in MLwiN: Results	78
5.4.1 Introduction	78
5.4.2 Results from Multilevel Continuous-Time Hazard Model	81
5.4.3 Summary	84
5.5 Use of Multilevel Survival Models in Previous Studies	85
5.6 Chapter Summary	88
6 Discussion: Findings from the Scottish Health Survey	91

6.1	Introduction	91
6.2	Summary of Findings	91
6.3	Limitations.....	98
6.3.1	Limitations of Data.....	98
6.3.2	Limitations of Variables and Analyses.....	101
6.4	Recommendations for Future Work	103
6.5	Implications of the Findings.....	104
6.6	Conclusions	105
7	Alternative Methods for Fitting Multilevel Survival Models to Large Datasets 106	
7.1	Introduction	106
7.2	Defining Different Risk Sets	106
7.2.1	Introduction	106
7.2.2	The Multilevel Discrete-Time Model.....	108
7.2.3	Assumptions.....	112
7.2.4	Estimation	113
7.3	Grouping According to Covariates.....	113
7.3.1	Introduction.....	113
7.3.2	Continuous-Time Models	115
7.3.3	Discrete-Time Models.....	119
7.4	Bayesian Survival Models	123
7.4.1	Introduction to Bayesian Multilevel Survival Models	123
7.4.2	Frailty Models.....	125
7.4.3	The Shared Frailty Model.....	126
7.4.4	Fitting Frailty Models in WinBUGS	130
7.4.5	Estimating the Parameters in WinBUGS.....	136
7.4.6	Monitoring Convergence in WinBUGS.....	139
8	Fitting Alternative Methods to the Scottish Dataset: Results.....	145
8.1	Defining Different Risk Sets	145
8.1.1	Multilevel Discrete-Time Models with Equal Intervals of Time	146
8.1.2	Multilevel Discrete-Time Models with Varied Intervals of Time ...	150
8.1.3	Summary: Defining Different Risk Sets	154
8.2	Grouping According to Covariates.....	155
8.2.1	Results from Grouping According to Covariates in Continuous Time 157	
8.2.2	Results from Grouping According to Covariates in Discrete Time.	161
8.2.3	Summary: Grouping According to Covariates.....	165
8.3	Bayesian Survival Models	167
8.3.1	Proportional Hazards Models using a Bayesian Approach.....	167
8.3.2	Fitting Frailty Models in WinBUGS	170
8.3.3	Fitting Bayesian Frailty Models to a Simulated Dataset	179
8.3.4	Reducing Correlation in the Weibull Model.....	183
8.3.5	Parameter Expansion in the Weibull Model	205
8.3.6	Summary: Bayesian Frailty Models.....	212
8.4	Chapter Summary.....	214
9	Applying Alternative Methods to a Larger Dataset	219
9.1	Introduction	219
9.2	Objectives using Swedish Data	219
9.3	Preliminary Analysis of Swedish Data.....	220
9.3.1	Descriptive Statistics	220
9.3.2	Missing Data.....	224
9.3.3	Results from Preliminary Analyses of Swedish Data.....	225
9.3.4	Summary of Preliminary Analyses of Swedish Data.....	230

9.4	Fitting Multilevel Survival Models to the Swedish Dataset.....	230
9.4.1	Multilevel Continuous-Time Survival Models	231
9.4.2	Multilevel Discrete-time Survival Models	232
9.4.3	Grouping According to Covariates	244
9.4.4	Bayesian Frailty Models.....	250
9.5	Conclusions: Results from the Swedish Data.....	262
9.5.1	Summary of Findings from the Swedish Dataset	263
9.5.2	Limitations of the Data.....	265
9.6	Conclusions: Suitability of Methods	266
10	Discussion.....	269
10.1	Introduction	269
10.2	Summary of Methodological Findings	270
10.3	Conclusions	274
10.4	Implications of the Findings.....	278
10.5	Limitations and Recommendations.....	280
10.5.1	Methodological Limitations and Recommendations	280
10.5.2	Other Limitations.....	282
10.5.3	Other Recommendations	283
Appendix 1:	12-Item General Health Questionnaire (GHQ-12).....	284
Appendix 2:	Checking the Proportional Hazards Assumption in the SHeS Data.....	285
Appendix 3:	Trace Plots and Gelman-Rubin Plots from SHeS Weibull Model ...	287
Appendix 4:	WinBUGS Code for Re-parameterised Model with all Covariates ..	291
Appendix 5:	Discrete-Time Groupings for Swedish Dataset	293
Appendix 6:	Checking the Proportional Odds Assumption in the Swedish Dataset	295
Appendix 7:	Fitting a Discrete-Time Model with Five Risk Sets to the Swedish Dataset.....	297
Appendix 8:	Trace Plots and Gelman-Rubin Plots from Swedish Weibull Model	299
Appendix 9:	WinBUGS code for the Weibull Model with Different Shape Parameters	303
References.....		304

List of Tables

Table 2.1 - Variables in the Scottish dataset.....	22
Table 2.2 - Variables in the Swedish dataset.....	23
Table 4.1 - Psychiatric admission following survey interview	43
Table 4.2 - Psychiatric admission following survey interview by survey year	44
Table 4.3 - Psychiatric admission following survey interview by number of prior admissions	45
Table 4.4 - Distribution of GHQ-12 score in SHeS	46
Table 4.5 - Psychiatric admission following survey interview by GHQ-12 score .	46
Table 4.6 - Results from multilevel logistic regression	53
Table 5.1 - Sample of SHeS Data before Expansion	69
Table 5.2 - Sample of SHeS Data after Expansion	69
Table 5.3 - Results from multilevel continuous-time hazard model	82
Table 5.4 - Summary of multilevel survival modelling literature with large datasets.....	86
Table 8.1 - Expanded dataset with equal discrete time intervals	147
Table 8.2 - Results from ML discrete-time models with equal intervals	148
Table 8.3 - Groupings for varying discrete time intervals.....	151
Table 8.4 - Expanded dataset with varying discrete time intervals	151
Table 8.5 - Results from ML discrete-time models with varying intervals	153
Table 8.6 - Expanded dataset when grouping according to GHQ-12 score in continuous-time	158
Table 8.7 - Results from ML continuous-time models grouped according to GHQ-12 score	160
Table 8.8 - Percentage reduction when grouping covariates for continuous-time models	161
Table 8.9 - Expanded dataset when grouping according to GHQ-12 score in discrete-time.....	162
Table 8.10- Results from ML discrete-time models grouped according to GHQ-12 score.....	164
Table 8.11 - Percentage reduction when grouping covariates for discrete-time models with varying intervals	165
Table 8.12 - Results from PH Models using a Bayesian Approach.....	169
Table 8.13 - Results from Weibull model	173
Table 8.14 - MC Error as a percentage of posterior standard deviation.....	177
Table 8.15 - Comparing intercept-only models between all-event and highly censored simulated datasets	180
Table 8.16 - Results from re-parameterised model fitted to simulated data ...	186
Table 8.17 - Results from Weibull model with re-parameterisation	200
Table 8.18 - Results of re-parameterised Weibull model with variance expansion	207
Table 9.1 - Percentage of events by cohort year	220
Table 9.2 - Percentage of events by socioeconomic risk factors.....	223
Table 9.3 - Results from preliminary analyses of Swedish data	226
Table 9.4 - Dividing time in the Swedish dataset.....	234
Table 9.5 - Discrete-time grouping for expanded dataset with 3 risk sets	235
Table 9.6 - Discrete-time grouping for expanded dataset with 7 risk sets	235
Table 9.7 - Results from fitting multilevel discrete-time models to Swedish data	236
Table 9.8 - Results from investigating the effect of cohort.....	243

Table 9.9 - Percentage reduction in expanded dataset when grouping according to covariates	245
Table 9.10 - Results from grouping according to covariates with Swedish data	246
Table 9.11 - Results from fitting Bayesian frailty models to Swedish data	252
Table 9.12 - MC error as a percentage of posterior standard deviation.....	255
Table 9.13 - Results from fitting re-parameterised Weibull model with variance expansion to the Swedish dataset	259

List of Figures

Figure 8.1 - Trace plots for GHQ-12 only model	174
Figure 8.2 - Trace plots for full model	175
Figure 8.3 - Gelman-Rubin plots for GHQ-12 only model	176
Figure 8.4 - Gelman Rubin Plots for full model	176
Figure 8.5 - Trace plots for intercept-only models from all-event & highly censored simulated datasets	180
Figure 8.6 - Gelman-Rubin plots for intercept-only models from uncensored & highly censored simulated datasets	181
Figure 8.7 - Trace plots for re-parameterised model fitted to simulated dataset with no censoring.....	189
Figure 8.8 - Trace plots for re-parameterised model fitted to simulated dataset with censoring	192
Figure 8.9 - Gelman-Rubin plots for re-parameterised model fitted to simulated dataset with no censoring.....	194
Figure 8.10 - Gelman-Rubin plots for re-parameterised model fitted to simulated dataset with censoring	195
Figure 8.11 - Trace plots for re-parameterised GHQ-12 model.....	201
Figure 8.12 - Trace plots for re-parameterised full model.....	202
Figure 8.13 - Gelman-Rubin plots for re-parameterised GHQ-12 model	203
Figure 8.14 - Gelman-Rubin plots for re-parameterised full model.....	203
Figure 8.15 - Trace plots for re-parameterised GHQ-12 model with variance expansion	208
Figure 8.16 - Trace plots for re-parameterised full model with variance expansion	209
Figure 8.17 - Gelman-Rubin plots for re-parameterised GHQ-12 model with variance expansion.....	210
Figure 8.18 - Gelman-Rubin plots for re-parameterised full model with variance expansion	210
Figure 9.1 - Date of event by birth cohort year.....	221
Figure 9.2 - Trace plots for 'Individual+Area' Model.....	253
Figure 9.3 - Gelman-Rubin plots for 'Individual+Area' model	253
Figure 9.4 - Trace plots for 'Individual+Area+Time*Cohort' Model	254
Figure 9.5 - Gelman-Rubin plots for 'Individual+Area+Time*Cohort' Model	254
Figure 9.6 - Trace plots for re-parameterised Weibull model with variance expansion	260
Figure 9.7 - Gelman-Rubin plots for re-parameterised Weibull model with variance expansion.....	261

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Author's Declaration

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1 Introduction

1.1 The Use of Event History Models in Public Health

When analysing medical or public health datasets, it may often be of interest to measure the time until a particular pre-defined event occurs, such as death from a particular disease. This time is known as the survival time. Event history models are applied when the outcomes are measures of duration. In general, the fundamental aim of event history analysis is to use data to provide estimates of the probability of surviving beyond a specified time. This probability is known as the 'survivor function'. It has been shown, however, that survival data are modelled more appropriately through the 'hazard function'. The term 'hazard' is used to describe the concept of the risk of 'failure' in an interval after time t , conditional on the subject having survived to time t [1]. With event history data, there may be information available on a number of explanatory variables suspected to have an effect on the time until event. The proportional hazards and accelerated lifetime models are the most commonly used models for regressing the time until event on potential explanatory variables in public health.

One of the main features of event history models is their ability to deal with incomplete observations of survival time, referred to as 'censored' observations. The most commonly encountered censoring mechanism in public health is 'right-censoring'. Right-censoring implies that it is known only that an individual has not experienced the event of interest by the end of a period of follow-up. Other types of censoring include 'left-censoring' and 'interval-censoring'.

For many outcomes, the health of individuals has been shown to vary between areas and this can also be true for event times. In such circumstances it is important that the data are analysed using multilevel models. Hence, in the case of event history data, multilevel event history models should be employed.

1.2 Introduction to Multilevel Modelling

There is a growing amount of research in epidemiology and public health into the relationship between characteristics of places where people live and health outcomes. This is creating widespread acceptance that health varies across geographic locations [2].

Although the focus on the importance of area variations in health outcomes has changed over time, the concept is not new. Initially, public health and early epidemiological investigations of infectious diseases were fundamentally ecological, and were interested in the associations of health and disease with environmental and community characteristics [3]. An example of this was John Snow's study of cholera, which concluded that geographical setting was key to the spread of cholera in London [4].

Conversely, between the mid 1940s to the early 1990s, modern epidemiology focused more on individual-level factors rather than environmental factors [5]. One reason for this shift was the increased prominence of chronic disease in this century, with research focusing mainly on behavioural and biological characteristics responsible for chronic disease [3]. A second reason concerned the 'ecological fallacy'. The ecological fallacy occurs when associations found at the group level are inferred to the individual level when, in truth, no such association exists [3, 6, 7]. The ecological fallacy arose as a result of ecological studies used in the 'pre-modern phase of epidemiology' [8].

Since the 1980s and early 1990s, there has been renewed interest in the importance of the effect of context on health outcomes [9]. The 'new public health' seeks to bring the focus of public health research 'back towards structural and environmental influences on health and health behaviours' [5]. Duncan, Jones and Moon [10] argued that, as well as recognising the health risks of the present day being associated with individual behavioural choices, they should also be regarded as being part of the broader social world. Health outcomes may be affected by contextual effects associated with a particular geographical location, or variations in health outcomes may be a result of compositional effects, whereby particular types of individuals, who are more

susceptible to poor health outcomes due to their individual characteristics, are clustered in particular geographical locations [11].

As discussed earlier, it is widely accepted that health varies across geographical locations. Instinctively, individuals within the same area tend to be more similar in health status than individuals from different areas [12]. This clustering of individuals within areas leads to a correlation of health outcomes for individuals within the same area, demonstrating the shared experiences of individuals within the same area [13]. This correlation structure leads to the violation of the assumption of independence required for common regression techniques, which in turn leads to underestimation of standard errors [13]. In addition, the finding of differences and relationships when they do not actually exist is also more likely [14].

Data that fall into hierarchies can be analysed using multilevel models, which account for the dependence of outcomes of people within the same area [12] [13]. Multilevel models allow the total variation in the response, which is measured at the individual level, to be partitioned into variation attributable to individual factors and variation that is attributable to differences between areas [7, 13]. The contribution of individual-level characteristics and area-level characteristics to the total variation in the response can then be measured simultaneously. Not only do multilevel models overcome the ecological fallacy defined earlier, they also overcome the ‘atomistic’ or ‘individualistic’ fallacy. The atomistic fallacy occurs when associations found between an outcome and an individual characteristic are inferred to the group-level, when in truth this association does not exist [3, 7].

Although multilevel modelling has appeared and reappeared over the last 50 years in a variety of forms [15], it was in the 1980s that notable developments in multilevel modelling occurred, in particular, in the field of educational research [16]. It is only in the last fifteen years that it has become more widely used in the field of public health [17], partly to deal with the problem of the ecological fallacy [18]. However, developments in statistical computing capabilities have now made multilevel models accessible to researchers from a number of different fields of research [19].

1.3 Objectives

When analysing event history data that fall into hierarchies, multilevel event history models should be used in order to account for the dependence of survival times of individuals nested within the same area. Although multilevel event history models have been developed, computational requirements mean that their use is limited for large datasets. This poses a problem for those working in the field of public health since datasets used for measuring and monitoring public health are typically large, coming from routine sources such as hospital discharge records or death records, or from survey sources. Additionally, depending on the outcome of interest and the length of follow-up, there may be relatively few events resulting in a large proportion of censored observations. Having many censored observations can also become problematic when estimating multilevel event history models.

The main objective of this thesis is therefore to investigate ways in which multilevel event history models can be developed to model large datasets. In particular, datasets with long periods of follow-up and cases where the outcome of interest is rare, implying a high proportion of censored observations, will be considered. Specifically, this research will consider limitations of existing software packages for fitting multilevel event history models and alternative strategies or software which may be applied instead.

1.4 Computing Hardware

All analyses in the thesis will be performed on a Dell OptiPlex 755 desktop computer with Intel® Core™ 2 Duo processor; processor speed 1.95 GHz and 2048 MB of RAM.

1.5 Overview of Thesis

The following chapter introduces datasets to which multilevel event history models will be fitted in order to investigate, firstly, the limitations of existing software packages for fitting these models and secondly, alternative strategies which could be applied.

Chapter 3 introduces the first research question which will be the main focus for the majority of the thesis. Background information detailing the context and specific aims to be investigated will be covered, as well as a thorough review of existing literature that has previously addressed this research question.

In Chapter 4, some initial investigations of the moderately-sized dataset being used to analyse the first research question are conducted. Specifically, this includes descriptive statistics and some preliminary analysis using multilevel logistic regression.

Chapter 5 introduces event history models, showing how a single-level model can be extended to incorporate random effects to fit multilevel models. A summary of existing software for fitting multilevel event history models is included, with a particular focus on MLwiN [20]. A detailed account of how MLwiN can be used to fit multilevel continuous-time event history models is given, along with some potential limitations of this package. This is demonstrated through fitting multilevel continuous-time event history models to the moderately-sized dataset being analysed to address the first research question. A brief summary of modelling strategies and software used in previous studies for fitting multilevel event history models to large datasets is also included.

Detailed conclusions for the first research question, as well as limitations of the dataset being analysed and the analyses performed to address this research question are considered in Chapter 6. Recommendations for future work and implications of the findings are also covered here.

Chapter 7 considers other potential methods which may be used as an alternative to fitting multilevel continuous-time event history models. In particular, other strategies which could be utilised in MLwiN are considered. The

latter part of this chapter discusses the use of WinBUGS [21] for fitting multilevel event history models using a Bayesian approach.

In Chapter 8, the alternative methods considered in Chapter 7 are fitted to the moderately-sized dataset being used to address the first research question. Results from fitting alternative methods are compared to the standard continuous-time models discussed in Chapter 5. The alternative methods are then assessed to determine whether they are adequate substitutes for fitting multilevel continuous-time event history models.

Chapter 9 introduces a much larger dataset which is then used to demonstrate how effective the alternative methods discussed in Chapter 7 are when fitted to a dataset with a larger number of individuals and a longer period of follow-up.

Finally, Chapter 10 discusses overall conclusions which can be drawn from the thesis. Methodological implications of the findings for those working in the field of public health are considered, as well as limitations of the research and recommendations for further research.

2 Data Description

2.1 Introduction

This chapter gives an overview of the datasets which will be used to investigate ways of fitting multilevel event history models. Two datasets will be analysed over the course of the thesis. The first is a moderately-sized Scottish dataset which will be used as a ‘training’ dataset for, firstly, investigating how multilevel continuous-time event history models can be fitted in MLwiN, along with the limitations of this software for fitting these models and secondly, for testing alternative strategies to fitting continuous-time models which can be utilised both in MLwiN, and in other packages. The Scottish training dataset will be the main focus for the majority of the thesis. Once effective alternative methods have been established using the training dataset, they will then be applied to a Swedish dataset consisting of a much larger number of individuals who were followed up for a much longer period of time compared with the Scottish dataset. As the Swedish dataset will only be used to see how effective alternative methods are when applied to a much larger dataset, the dataset and research questions to be analysed will not be considered in as much depth as the Scottish dataset.

2.2 The Moderately-Sized Scottish Dataset

This section introduces the Scottish dataset which will be used as the training dataset as described in Section 2.1 above. The data come from the 1995 and 1998 Scottish Health Surveys (SHeS), and were linked to all death records and psychiatric hospital admission records (Scottish Morbidity Record 04 (SMR04)) [22].

The 1995 and 1998 Scottish Health Surveys are the first two of a series of ongoing general health surveys being conducted in Scotland. Before the introduction of the Scottish Health Survey (SHeS) in 1995 there was a paucity of systematic information on health and health-related behaviour available in

Scotland to allow researchers to investigate reasons for variations in mortality and morbidity in the Scottish population [23]. The series of surveys, commissioned by The Scottish Executive Health Department (formerly The Scottish Office Department of Health) was designed to rectify this lack of knowledge.

The SHeS is modelled on the annual Health Survey for England in terms of the core questions and measurements recorded. Therefore, in addition to allowing the investigation of explanations for variations in mortality in Scotland, differences between Scotland and England may also be investigated.

A wide range of information on health-related factors (e.g. long-standing illness, recent diagnoses, prescribed medicines), behavioural variables (e.g. smoking, physical activity) and biological measurements (e.g. blood pressure, BMI) were recorded by the survey via an interview and a nurse visit [24]. Information on deprivation and socioeconomic characteristics was measured both at the individual-level and the household-level. The sample was designed to provide a nationally representative sample of the working-age population of Scotland in private households and is based on a stratified multistage random sample design covering all of mainland Scotland as well as the larger inhabited islands [23, 25]. Postcode sectors within Scotland were ordered by region (seven regions defined by Health Board) and deprivation (using the Carstairs index of deprivation [26]), with 312 postcode sectors then being selected each year. Within the 312 sampled postcode sectors, 14 358 and 15 288 addresses were selected for the 1995 and 1998 surveys respectively using the Postcode Address File (PAF) [23, 25]. There were slight differences between the 1995 and 1998 surveys when proceeding to select households and individuals from the random sample of addresses. In the 1995 survey, one person aged 16-64 was randomly selected for inclusion at each address containing a private household. However, in the 1998 survey up to three private households at each address could be selected. The age limits were also changed so that anyone aged 2-74 was eligible for inclusion. In each private household one person aged 16-74 and up to two children aged 2-15 were randomly selected for inclusion. However, in this thesis, analyses will be based only on subjects aged 16-74 years, i.e. children will be excluded. This multistage clustered design is a commonly used sampling method in national

surveys and is more cost-effective than designs without clustering, such as simple random sampling [27].

Data from the Scottish Health Survey were obtained for use in the thesis by means of a data application request to the Information and Services Division Scotland (ISD Scotland). On applying for the survey data, all psychiatric hospital admission records (SMR04), as well as all death records were requested in the form of a linked dataset. The SMR04 is used to collect patient based data on day cases and inpatient admissions, readmissions and discharges from psychiatric hospitals and units.

Linkage of the 1995 and 1998 SHeS data to Scottish hospital admission records and death records began in 2004 [27]. For those survey respondents who gave permission to be linked to the NHS administrative database, survey data were linked with all Scottish hospital records and death records from the year 1981 to 2004 [27]. Linkage was successful with around 92% of respondents in each of the 1995 and 1998 surveys agreeing to have their survey data linked to the NHS administrative database [24]. The linkage procedure is summarised briefly as follows [28]. For all respondents who agree to linkage, the National Centre for Social Research (NCSR) send a datafile containing details of respondent's name, postcode, date of birth and year of participation in survey, along with an encrypted serial number, to ISD Scotland for linkage with hospital records and death records using probability matching techniques [29]. Following anonymisation, these linked records are then forwarded to NHS Health Scotland (formerly the Public Health Institute of Scotland). In addition, NCSR provide NHS Health Scotland with a datafile containing all survey data and the same encrypted serial number. The encrypted serial number thus allows merging of survey data and the linked hospital and death records. The final merged dataset, which does not include the encrypted serial number, is then sent back to and stored by ISD Scotland. A primary benefit of data linkage includes being able to investigate relationships between risk factors measured in the health survey and hospital admissions or mortality [24]; however, there are also some weaknesses associated with using linked datasets for analysis. These will be considered in Section 6.3.1.

When requesting the linked datasets from ISD Scotland, a description of all survey variables required was also included in the application. Although many variables were available, only those shown in Table 2.1 below were requested.

Table 2.1 - Variables in the Scottish dataset

Individual-Level Risk Factors				Area-Level Risk Factors
Demographic	Socioeconomic	Psychosocial	Lifestyle	
Sex	Living Alone	GHQ-12 Score	Smoking Status	Carstairs Score
Age	Children	Self-Assessed General Health	Alcohol Consumption	Type of Area
Marital Status	Social Class of Chief Income Earner			
	Home Ownership Status			
	Car/Van Access			
Others	Benefits		Physical Exercise	
	Age Finished Education			
Height	Top Academic Qualification			
	Employment Status			

The data were received from ISD Scotland in April 2006. All cleaning and merging of the 1995 and 1998 linked datasets was done at this time for a dissertation submitted in August 2006 as part of the University of Glasgow Master of Public Health degree [30].

2.3 The Larger Swedish Dataset

This section introduces the Swedish dataset being used to test the effectiveness of the alternative methods when fitted to a much larger dataset. Only a brief overview is given here since this dataset is not the main focus of the thesis.

The Swedish dataset consists of two birth cohorts from the years 1972 and 1977, containing 99458 and 86505 individuals respectively. Individuals were followed up until at least 2003 with the last date of follow-up in 2006. It is clear from this that the Swedish dataset is much larger than the Scottish dataset, in terms of both the number of individuals and the length of follow-up time.

Like the Scottish dataset, the Swedish dataset is hierarchically structured, with the 185963 individuals nested within 2596 parishes, which are in turn nested

within 280 municipalities. Early-life socioeconomic variables at both the individual-level and the higher-levels were available, as displayed in Table 2.2.

Table 2.2 - Variables in the Swedish dataset

Individual-Level Variables		Higher-Level Variables
Demographic Variables	Socioeconomic Variables	
Sex Birth cohort year	Father's social class in 1980 Household income quintile at birth Housing tenure at birth	Economic Region

The Swedish dataset is provided courtesy of Dr Göran Henriksson, University of Gothenburg.

3 Mental Health and Psychiatric Admissions in Scotland

A current and increasing health problem in Scotland is that of mental illness. Using the linked Scottish Health Survey (SHeS), this thesis will investigate those at risk of mental health problems in Scotland. This chapter provides an overview of the extent of mental health problems in Scotland, and how mental health problems are recorded and detected. Later sections of this chapter provide a review of the literature for risk factors associated with poor mental health. The final section of this chapter sets out the objectives to be considered when analysing the SHeS data.

3.1 Introduction to Mental Health in Scotland

The World Health Organisation (WHO) defines health as ‘a state of complete physical, mental and social well-being and not merely the absence of disease or infirmity’ [31]. The Scottish Public Mental Health Alliance [32] noted that, throughout the last century, there was an improvement in physical health in Scotland and remarked that even mortality from illnesses such as heart disease and cancer declined. However, they observed that the pattern of disease in the industrialised world is changing, with poor mental health, as opposed to poor physical health, being the main burden of ill-health in Scotland today. In order to improve health to comply with the WHO’s definition, the new challenge for the 21st century must be to focus on improving mental health and well-being.

In Scotland, it has been estimated that one in four people will experience problems with mental wellbeing during their lifetime, and a recent survey revealed that 62% of Scots knew of someone who had been diagnosed as being mentally ill [33]. To highlight the costs of mental health problems to society and the economy in Scotland, a report entitled ‘What’s it Worth?’ was launched in 2006. The report found that the total cost of mental health problems in Scotland in 2005 was £8.6 billion, which was more than the total amount spent by the National Health Service (NHS) in Scotland for all other health conditions

combined [34]. The document 'With Health in Mind: Improving mental health and wellbeing in Scotland' [32] provides a further insight into the costs of mental health problems in Scotland, in particular, the cost to industry. It reported that around 3 in 10 employees experience mental health problems each year. Further research commissioned by the Scottish Association for Mental Health [35] reported that the cost of absence as a result of mental health problems to Scotland's employers was around £360 million.

Definitions of mental disorder expand to include anything from conditions such as depression and schizophrenia to alcohol and drug abuse. The terminology used to describe poor mental health varies considerably and is not clear-cut [36]. In general, mental disorder is divided into two categories, namely neurotic and psychotic disorders. Neurotic disorders, such as depression, are much more common than psychotic disorders, and indeed, nowadays, are referred to as 'common mental health problems' [37]. The World Health Organisation [38] predicts that, by the year 2030, 'depression will become the single highest contributor to the overall disease burden' in high-income countries. However, psychotic disorders, such as distortion of a person's perception of reality, are much more severe and can be viewed as 'mental illness' as opposed to a mental health problem [36]. Duration and severity of symptoms are two elements considered when making the distinction between mental health problems and mental illness, with mental health problems usually being shorter in duration and less severe than mental illness [36]. In this thesis, no distinction will be made between mental health problems and mental illness, and the term 'mental disorder' will be used to encompass both aspects.

In response to the problem of mental disorder in Scotland, 'The National Programme for Improving Mental Health and Wellbeing' [39] was initiated in 2001 with the vision 'to improve the mental health and well-being of everyone living in Scotland and to improve the quality of life and social inclusion of people who experience mental health problems'. This programme is important in terms of the Scottish Government's commitment to improving health in Scotland [40]. The 'With Health in Mind: Improving mental health in Scotland' [32] document also acknowledges that positive mental health is 'a fundamental resource for everyday life and the basis of physical, mental and social wellbeing for everyone'. Both of these documents recognise that improving the mental health

of the population may in turn impact on physical health status. The World Health Organisation also reported evidence of the link between mental and physical health and illness [38, 41] and therefore, if promoting positive mental health in Scotland can also improve physical and social wellbeing, then this is a step forward in achieving the World Health Organisation's definition of health.

3.2 Recording and Detecting Mental Disorder in Scotland

In Scotland, most of the information on mental health comes from acute and psychiatric hospitals, where data are collected at the time of admission to, and discharge from, hospital on all patients [42]. Therefore, it seems reasonable to use psychiatric admission as an indicator of poor mental health in Scotland. A discussion of how information on psychiatric admissions in Scotland is obtained, as well as its linkage with the SHeS, was given Section 2.2.

Admissions to psychiatric facilities in Scotland are classified into one of three categories: a first admission if 'patients have not previously received psychiatric inpatient care'; a readmission if 'patients are readmitted following a break from psychiatric care'; or a transfer if patients have a 'direct transfer from another psychiatric hospital or from one consultant to another within the same hospital' [42]. Since 1996, patients have been further classified into one of five mental illness specialities on admission to psychiatric facilities - either general psychiatry, psychiatry of old age, adolescent psychiatry, child psychiatry or forensic psychiatry.

Up-to-date figures on psychiatric hospital activity in Scotland are published by the Information and Services Division (ISD). Their latest statistics reported that there were a total of 24294 admissions to mental health hospitals during the year ending 31 March 2007 [43]. Twenty-seven percent of this was for first-ever admission to psychiatric inpatient care, fifty-eight percent for readmissions, and ten percent for transfers from another psychiatric hospital. Admission type for the remaining five percent was unknown. The figures reported here continue a downward trend, and represent a 16% reduction in the number of admissions since 2003 [44]. The downward trend in psychiatric admission, for those

diagnosed as mentally ill, may represent a shift away from inpatient psychiatric care towards caring in the community. Indeed, the World Health Organisation recommends the closure of large psychiatric hospitals, with treatment instead being offered in primary care centres and other community-based settings [38].

Although the World Health Organisation advise that primary care services are usually the most affordable option for providing mental health care, they acknowledge that, worldwide, there is a significant gap between the prevalence of mental disorders and the number of people receiving treatment [38]. They reported that at least one in four patients who visit a health service has some kind of mental disorder. However, most of these go undiagnosed. A number of self-administered questionnaires have been developed to aid the detection and prediction of mental disorder, one of which is the General Health Questionnaire (GHQ). A discussion of the GHQ is given in the following section (3.2.1).

3.2.1 The 12-item General Health Questionnaire (GHQ-12)

3.2.1.1 The Use and Scoring of the GHQ-12

It is accepted that the GHQ is one of the most widely used self-administered questionnaires when assessing for possible psychiatric morbidity [45-47]. The GHQ was designed to detect breaks in normal function, rather than lifelong traits, and only detects mental disorders of less than two weeks' duration [48]. Several versions of the GHQ are available, each of a different length. However, the shortest version (GHQ-12) comprises twelve questions based on general levels of happiness, anxiety and depression. For each of the twelve items, respondents rate their recent experiences of that particular symptom or behaviour using a four-point scale ranging from 'less than usual' to 'much more than usual'. There are then two possible ways in which this four-point response scale is scored: the original scoring method, known as the GHQ or binary method; or the Likert method. Goldberg and Williams [48] and Hardy et al. [49] give a comprehensible summary of the two methods of scoring. A copy of the GHQ-12 can be found in Appendix 1.

There are a number of reasons why the shorter GHQ-12 is favoured over the longer versions, the first reason being that it takes less time to complete (between 2 and 5 minutes) than the longer versions, and so its use is more appealing in busy clinical settings [47, 50, 51]. Secondly, van Hemert et al. [46] found that individuals were likely to answer more affirmatively when shorter versions of the GHQ were used. Thirdly, physical illness is thought to have an influence on scoring in the GHQ, with higher scores being obtained for those who are medically ill [46, 48]. The GHQ-12 eliminates this problem as all questions regarding somatic symptoms were removed from this version [46, 48]. Finally, although the GHQ-12 contains fewer items than the longer versions, it has been found that this shorter version is similar to the longer versions in detecting psychiatric cases [46, 50, 52].

As well as being used as a self-administered screening test to detect psychiatric disorders in community settings and non-psychiatric clinical settings or as part of a two-stage process to make clinical diagnoses, the GHQ may also be used in survey research [48]. In fact, it is the GHQ-12 that is used in the Scottish Health Survey (SHeS) to assess the psychosocial health of respondents [23, 25]. Informants in the SHeS were asked to complete the GHQ-12 in the form of a self-completion booklet at the end of the main survey interview in order to detect any possible psychiatric morbidity in the few weeks prior to interview.

In order to classify subjects as having a potential psychiatric disorder, a threshold score between 0 and 12 must first be defined. In his original validity study of the GHQ-12 in the UK in 1972, Goldberg found that a score of 1 or 2 was the optimal threshold score [45, 50]. However, there are many issues which should be considered when selecting a threshold score, and these issues have been considered by a number of different authors [45, 46, 48-55]. Lewis and Araya[45] wrote that the threshold score should be chosen to 'maximise the sensitivity and specificity of the GHQ'. Sensitivity refers to 'the probability of testing positive if the disease is truly present' and specificity refers to 'the probability of screening negative if the disease is truly absent' [56]. It is generally accepted that the threshold score needed to maximise the sensitivity and specificity varies considerably between different settings, cultures and populations [45, 46, 48, 51, 52, 54, 55]. Some authors recommend that the mean GHQ score in a specific population provides a rough guide to the best threshold

score[53, 57]. However, Willmott et al. [55] argued that the mean value may be more sensitive to skewness, and instead recommended that the median GHQ score be a more reliable guide of threshold score than the mean. Most agree, however, that the GHQ be tested in the intended target population in order to establish the best threshold for that particular setting [46, 48, 52].

3.2.1.2 Other Issues with the GHQ-12

A common issue arising from the literature in terms of the GHQ is that its use is only recommended for detection of minor psychiatric disorder such as depressive symptoms and anxiety [49, 51, 58]. However, it has been discussed that it may not detect chronic neurotic illness [59], but as was discussed in Section 3.2.1.1, it was only intended that the GHQ would detect breaks in normal function, rather than lifelong traits [48].

A number of studies have been conducted to assess the performance of the GHQ. This is usually represented in terms of specificity, sensitivity and positive and negative predictive power [60]. It has been argued that the GHQ has low positive predictive value [61] and a high rate of false positive results, and that to overcome this the GHQ should be combined with other screening instruments [47, 61]. However, Goldberg and Williams [48] argued that there was never any intention that the GHQ should possess predictive validity.

A bias which may be associated with the GHQ is reporting (or responder) [45, 49, 58]. It has been shown that some people may give false answers to questions, and therefore those who are mentally distressed would not reach caseness and be diagnosed [45, 49]. However, to overcome this bias, the GHQ was designed in such a way as to ask questions on both negative and positive aspects of mental health, and, when the original binary GHQ scoring method is applied, those who answer as having 'no change' in recent behaviour or symptoms to the negative items are still scored, thus contributing to overall score [49]. In other words, problems associated with 'middle users' (i.e. respondents answering 'no change' in recent behaviour or symptoms) are avoided [48].

There are some references in the literature acknowledging that the GHQ correlates well with other self-administered questionnaires. Hardy et al. [49] investigated the correlation of the GHQ-12 with questionnaires such as the Brief Screen for Depression and the Warr Depression scale, and found high to moderate correlations of 0.70 and 0.63 respectively. Goldberg and Williams [48] also reported results from investigating the correlation of various versions of the GHQ with other self-administered questionnaires. Published results from the Scottish Health Surveys also reported a strong relationship between GHQ-12 and self-reported health with a poor rating of self-assessed general health being related to a high score on the GHQ-12 [23, 25]. It may therefore be necessary to take this supposedly high correlation between GHQ and self-reported health into account when analysing the SHeS data. This notion is discussed further in Section 3.5.

In Section 3.2.1.1 it was discussed that the threshold score for the GHQ may vary considerably between different settings and cultures. However, there are also a number of other factors which have been noted as having an effect on the validity of the GHQ-12. The most common discussions highlighted in the literature were regarding the effect of sex, age and socioeconomic status on GHQ [45, 50, 51, 58, 62]. In terms of the effect of sex on GHQ score, Donath [51] reported women as obtaining higher scores on average than men; however, this conclusion was not supported by Banks et al. [62], who reported no difference in scores obtained between the sexes. In terms of validity with regard to the effect of sex, Goldberg et al. [50] found no difference in the validity characteristics between males and females; however, they noted that this finding conflicted with that of Mari & Williams [63], who found that the GHQ worked better with females than with males. When considering age in terms of its effect on score and validity, Banks et al. [62] found no significant relationship between age and score, and Goldberg et al. [50] reported no effect of age on the validity characteristics. There is a wide range of information available on the association of socioeconomic circumstances and GHQ. In their recent paper investigating socioeconomic circumstances and common mental disorders (as measured by the GHQ-12), Lahelma et al. [58] highlighted reporting bias as a problem with those in lower socioeconomic positions, especially amongst lower-class men. The main findings from this paper indicated that childhood and adulthood economic

difficulties were strongly associated with a GHQ-12 score of 3 or more; however, they reported generally non-existent associations between a GHQ-12 score of 3 or more and the more widely used measures of socioeconomic status (e.g. education, occupational class, home ownership). In terms of validity, an early study by Banks et al. [62] found that GHQ-12 scores were not sensitive to job level (e.g. blue collar, managerial, etc). This was supported by Goldberg et al. [50] who found that validity characteristics were not influenced by educational level (if it can be assumed that educational level is a proxy for job level). However, both Goldberg et al. [50] and Lewis and Araya [45] reviewed studies by other authors who found an effect of educational level on the validity of the GHQ-12, in that the less well educated were more likely to be false positives on the GHQ [63, 64]. An extremely comprehensive review of the effects of a range of demographic and personality variables on the GHQ in different cultural settings, as found by a variety of authors, is also given by Goldberg & Williams [48]. Taking all of the above arguments into consideration, it may be sensible to adjust for such risk factors when analysing the SHeS data.

3.3 Risk Factors for Psychiatric Admission

It was discussed in Section 3.2.1.2 that GHQ-12 score could be affected by a number of factors, such as sex, age and socioeconomic status. If GHQ-12 score varies between populations, and if the GHQ is taken as a measure of potential psychiatric morbidity, then this could imply that different populations may be at different degrees of risk of developing psychiatric morbidity, and thus possibly experiencing a psychiatric admission. This section will review the literature on possible risk factors for mental disorder in order to establish which risk factors could affect the likelihood of psychiatric admission.

3.3.1 Demographic Predictors

There is a large body of literature available on the investigation of differences in rates of mental disorders by demographic risk factors such as sex, age and

marital status. It is generally accepted that each of these variables, either when considered separately or when interacting with each other, may be an important selection factor for the prevalence of psychiatric disorder and/or psychiatric treatment [65, 66]. As shown in Table 2.1 (Section 2.2), data were available on the sex, age and marital status of respondents of the SHeS. A literature review of the association between each of these three variables and the prevalence or treatment of psychiatric disorder was conducted, and the findings are considered here.

Debates over the relationship between sex and psychiatric disorder arose in the 1970s, and at this time it was generally accepted that women had higher rates of psychiatric disorder [67-70]. However, since then, the evidence surrounding the debate has grown, and led to differing conclusions in terms of the prevalence of psychiatric disorder. A study by Zent [68] could not support past theories of women having higher rates of mental disorder, but Zent also commented that this did not necessarily imply that males had higher rates. In 1985, a study by Jenkins [71] reported a less than two percent difference in the prevalence of minor psychiatric morbidity between the sexes, and also went on to conclude that there were no sex differences in the prevalence following adjustment for age, education, occupation and social environment.

As well as the debate surrounding differences in the prevalence of psychiatric disorder between the sexes, there is also controversy on differences in service utilisation i.e. admission to psychiatric facilities. A review of the literature into admissions demonstrated that results were inconclusive. It has been reported that, although there may be gender differences in the prevalence of psychiatric morbidity, there was no evidence to suggest that women had higher rates of treated disorder [65]. This finding was also supported by others. Kirshner and Johnston [72] concluded that there was no significant effect of sex on admission in the USA, either when considered additively or in combination with other demographic and socioeconomic risk factors. A study conducted on a Swedish cohort by Timms [73] also concluded that males and females had the same overall incidence of hospitalisation with a psychiatric diagnosis. The conclusions of Kirshner and Johnston and Timms were both based on studies conducted outside the UK; however, a study by Jarman et al. [66] reported similar national psychiatric admission rates for men and women in the UK. More specifically, a

study conducted using the Scottish Health Survey data by Stewart [30] found that sex had no significant effect on first psychiatric admission, following adjustment for a range of other risk factors.

There are a number of studies, however, that do report differences in psychiatric admission between the sexes. The earliest such study to be reviewed was that of Zent [68]. Zent concluded that the rates of first admissions in the USA were higher in males than in females. More recent studies were carried out by Saarento et al. [74] in Finland and Thompson et al. [75] in England. Again, both of these studies reported higher admission rates for males than for females, even following adjustment for various other risk factors [74]. These three studies all concluded that psychiatric admission rates were higher in males; however, both Zent and Saarento et al. discussed that this finding may occur as a result of males suffering from disorders, or exhibiting behaviour, that more often require hospitalisation than females. This suggestion will be considered further in Chapter 6.

A few studies consider the effects of age on psychiatric disorder. Rushing [76] reported that the rates of most types of mental disorder were highest in adults aged 20-34 years, and decreased thereafter. Indeed, Fox [65] found that rates of treated mental illness peaked around 25-44 years before declining. Recent studies, however, do not support this notion. Although Mattioni et al. [77] found a significant univariate effect of age on psychiatric admission; this effect did not remain significant when other risk factors were considered in addition. This finding is consistent with that of Stewart [30] who reported no significant effect of age on first psychiatric admission following adjustment for a range of other risk factors.

Another important demographic predictor of prevalence of psychiatric disorder and rates of admission is marital status. As with sex, there is a large body of literature available on the association of marital status and psychiatric disorder. However, unlike sex, where results are inconsistent, studies investigating marital status generally lead to the same conclusion, and indeed Martin [78] and Rushing [76] acknowledge that the relationship between marital status and psychiatric disorder is one of the most persistent and consistent findings. Of the studies investigating the effect of marital status reviewed here, it was found by all that

married persons were at the lowest risk of psychiatric disorder and had the lowest likelihood of admission [30, 65, 76, 78-81]. There is, however, strong evidence of an interaction between marital status and sex, with it being suggested that married women are at higher risk of psychiatric disorder and admission than married men, and vice versa for unmarried persons [65, 79, 80, 82, 83]. Indeed, it was acknowledged by Gove [84] that ‘...the data on mental illness...clearly suggest that in modern Western industrial society marriage is more beneficial to men than women’ [85]. However, Tweed & Jackson [82] maintained that, although married females may be at a higher risk of psychiatric disorder than married males, they (married females) were still at a lesser risk than persons of any other category of marital status.

3.3.2 Socioeconomic Predictors

It has been inferred by some that there is a firmly established association between socioeconomic position and psychiatric disorder, with lower socioeconomic position being associated with a higher risk of mental disorder [73, 86, 87]. However, as acknowledged by Rushing and Ortega [88], these inferences do not distinguish between types of disorder. Although it seems to be agreed that severe mental disorders, such as schizophrenia and major depression, are unequally distributed by socioeconomic position, with the prevalence of severe mental disorder being higher among those in lower socioeconomic position [58, 66, 89, 90], a review of the literature has highlighted inconsistencies in conclusions regarding the association between socioeconomic position and common mental disorders. Whilst Rodgers [91] and Weich et al. [92] ascertain that common mental disorders (also known as neuroses), such as anxiety, are much more common in persons of lower socioeconomic position; Dohrenwend [93], Weich & Lewis [94], Lahelma et al. [58] and Skapinakis et al. [95] all contend that there are inconsistencies in the evidence on socioeconomic differences in common mental disorders.

Some authors focused purely on reviewing literature on the association between socioeconomic position and admission to psychiatric hospital, and all recognised a long-standing association between low socioeconomic position and admission

to psychiatric hospital [96, 97]. However, an admission to psychiatric hospital may be regarded as an outcome of more severe mental disorders. This notion will be discussed further in Chapter 6.

A wide range of different variables are used in studies to measure socioeconomic position, and conventional measures normally include social/occupational class, education, income, material circumstances (such as home and car ownership) and employment status [58, 86, 90, 98, 99]. Kessler [86] proposed that, when one is measuring socioeconomic position, either one of these measures could be used, or two or more could be used together. However, he debated that the same association was found no matter which procedure was employed. This is not supported by Lahelma et al. [58], who suggested that there may be variations in the association between socioeconomic position and mental disorder depending on which measure is adopted. Apart from income, data were available on all of the measures listed above in the Scottish Health Survey (see Table 2.1 in Section 2.2 for a full list of variables).

Several studies have investigated the role of social class as a measure of socioeconomic position, and its association with mental disorder and psychiatric admission. The results have been varied. Studies by Weich and Lewis [94], Belek [98] and Lahelma et al. [58] found an association between low social class and common mental disorder, as measured by the GHQ. Halldin [83] found that a higher percentage of respondents in the lowest social class in their study carried out in Sweden had a psychiatric diagnosis; however, this finding was not investigated using formal methods. In relation to psychiatric admissions, Thornicroft [89] and Jarman et al. [66] found moderate positive correlations between low social class and admission to psychiatric hospital. In contrast to these findings, studies by Rodgers [91], Weich et al. [92] and Skapinakis et al. [95] all reported no association between social class and common mental disorder. It was also found by Stewart [30] that social class was not associated with psychiatric admission, following adjustment for a range of other risk factors.

There have been some disputes over the reliability of social class as a measure of socioeconomic inequality [100], especially in terms of its precision [86], and Fryers et al. [90] agreed that it does not apply well to women, students, armed

forces, retired or unemployed persons. They went on to suggest that education, employment status and material circumstances may be more precise and more easily definable measures of socioeconomic position, as well as being representative of factors which contribute to overall social class.

It has been demonstrated that education is a good marker of long-term economic position [90], and it has also been noted that education affects employment, which, in turn, may affect income [58]. In the Scottish Health Survey, data were available on age at which education was completed and highest academic qualification attained. It is expected that both of these variables are highly correlated, although it is recommended by Fryers et al [90] that years spent in education may be a more comparable measure than highest academic qualification attained, especially across different cultures. Both Kessler [86] and Belek [98] found an association between education and psychological distress, and Rushing & Ortega [88] found a decreasing trend in psychiatric admission rates as the number of years spent in education increased. However, this was not supported by Stewart [30], who reported no association between education and risk of psychiatric hospital admission.

As discussed above, employment status is one of the commonly used measures of socioeconomic position, and there is a long history of interest in the relationship between employment status and mental disorder, with evidence suggesting that unemployment is causally associated with common mental disorders [92, 101]. A number of more recent studies have continued to investigate the association of employment status and psychiatric admission. Studies by Kammerling & O'Connor [96], Koppel & McGuffin [87] and Stewart [30] reported strong associations between unemployment and psychiatric admission, with the first study reporting that 'unemployment rates alone explained over 90% of the variation in standardised admission ratios'. However, Kammerling & O'Connor did point out that including persons aged over 65 years would underestimate the power of this relationship. This statement suggests that employment status may not be a useful predictor in older respondents.

Income is another of the conventional measures of socioeconomic position. However, the accuracy of this as a measure has been questioned by some. Fryers et al. [90] advised that income data obtained from questionnaires may not

always be reliable, and Carter et al. [102] also argued that it may be influenced by short-time changes in employment. Instead, both of these studies agreed that ‘wealth’ was a better measure than income, with Fryers et al. suggesting that wealth may be measured by recording material standard of living, perhaps in terms of car and home ownership. Data were available on both car and home ownership in the Scottish Health Survey. Indeed, a number of studies have investigated the association between mental disorder and car and home ownership. In their study predicting psychiatric admissions in Wales, Koppel & McGuffin [87] found that the best predictor of admission for most types of psychiatric disorder was not having a car. Two other reviewed studies also echoed this finding. Both Jarman et al. [66] and Thornicroft [89] found moderate positive correlations between not having a car and psychiatric admission. In terms of home ownership, however, neither Lahelma et al. [58] nor Stewart [30] found an association between home ownership and common mental disorder as measured by the GHQ [58], or psychiatric admission [30].

3.3.3 Lifestyle Predictors

In the SHeS dataset, information was also available on a number of ‘lifestyle’ variables, namely, smoking status, physical exercise and average alcohol consumption per week. There has been a recent increase in interest on the effect of such lifestyle predictors on mental disorder, and this section will provide a brief review of some of the available literature.

It is well established that smoking is a risk factor for many diseases, such as lung cancer [103, 104]; however, its link with mental disorder is also becoming well-recognised. It is known that persons with mental disorder have elevated tobacco use; nevertheless, the causal pathway is not clear [105]. In the past it was assumed that mental disorders caused smoking, but recent evidence has also suggested that smoking may increase the risk of mental disorder [105-107]. The reviewed literature revealed that smoking was associated with common mental disorder [105, 107, 108], and that this association remained, even after adjustment for further risk factors [107, 108]. Both Rasul et al. [108] and Araya et al. [107] also reported that the risk of disorder increased with increased

smoking habit; however, this was not found by Cuijpers et al. [105]. The findings for severe mental disorder, such as major depression, are inconsistent. It has been noted by some that the risk of major depression is higher in smokers [103, 106], and, although Breslau et al. [106] confirmed this in their study in the USA, this association was not found by Cuijpers et al. [105]. Stewart [30] reported a significant increase in the likelihood of psychiatric admission, which may be a measure of severe mental disorder, in current smokers, and found that this increase remained significant following adjustment for a range of other risk factors.

Between the late 1980s and early 1990s there was a vast increase in interest in the topic of exercise and mental health [109], with previous studies suggesting that exercise or physical activity was associated with mental disorder, and in particular with depression [109-111]. A dose-response relationship between activity level and risk of depression was also reported by Paffenbarger et al. [111, 112], with those participating in high activity being at a greater reduced risk of depression. Although a relationship has been established for depression, a common mental disorder, there is an absence of information available on the association of exercise or physical activity with severe mental disorder and hence possibly with psychiatric admission if those with a severe mental disorder are more likely to be admitted to psychiatric hospital than those with a common mental disorder. A more comprehensive review of the evidence of what is known about exercise and mental illness can be found in the inaugural edition of the 'Mental Health and Physical Activity' journal [113].

There is evidence to suggest that prolonged alcohol abuse can cause certain mental disorders; however, as with smoking, there are two types of cause-effect relations that should be considered - whether alcoholism is a result of mental disorder, or whether high alcohol consumption leads to mental disorder [114, 115]. In a study of young Swedish males, Andréasson & Allebeck [115] found a strong association between high alcohol consumption and psychiatric admission, which remained after adjustment for other variables, but they did remark that, even though the independent effect of alcohol consumption remained following adjustment for a range of other factors, it was not the strongest predictor of psychiatric admission. However, a study by Bernadt & Murray [114] considered various diagnoses at admission, and found that only those admitted for

alcoholism had a significantly higher mean alcohol consumption than those admitted for other diagnoses, such as major depression and personality disorders. In terms of common mental disorder, a Mexican study by Arillo-Santillan et al. [107, 116] reported an association between alcohol and depressive symptoms.

3.4 Area Variations in Mental Illness

Winkelstein [18, 117] proposed that ‘ecological factors may be the most important determinants of the health and disease status of a population’. In relation to this, Section 1.2 summarised the widely accepted notion that health varies across geographical location and reviewed the renewed interest in the importance of context on health outcomes. Although there is a long history of interest in the effect of place on mental health, with work by Faris and Dunham dating back to 1939 [118], the evidence is limited [119-123], particularly in Britain [124], and a review of the literature on the effect of place on mental health highlighted inconsistencies in the available evidence. Dupéré & Perkins [121] stated that there had been very little examination of the contextual risk factors, i.e. the specific attributes of a place, in relation to mental health, and that contextual risk factors, if they were investigated, appeared to most commonly include urban/rural status [123, 125-128] or aggregated compositional risk factors, such as mean/median (household) income [123, 129], unemployment rate [118, 120, 123, 130, 131], percentage receiving a range of benefits [118, 122, 132, 133], ethnic minority composition [118, 120, 125, 131, 134], proportion living in poverty [118, 123, 134] and social fragmentation/cohesion [121, 128, 134-136], or indices measuring area-based deprivation constructed from compositional risk factors, such as, an index of multiple deprivation/Townsend score/Carstairs index [119, 128, 133, 137-140].

Most of the literature reviewed here used multilevel models in order to observe the variation of measures of mental disorder at area/neighbourhood level as they adjusted for compositional and contextual risk factors. However, a few of the studies failed to employ multilevel modelling techniques, even though their

data were hierarchical; these including Paykel et al. [126] and Allardyce et al. [128], who both had postcode sector information, Sundquist et al. [127], who had small-area market statistics (SAMS) information, and Harrison et al [131], who had health district information. As pointed out in Section 1.2, ignoring the hierarchical structure of data can lead to underestimation of standard errors, and therefore conclusions drawn in these studies may be misleading. With this in mind, the remainder of this section only reviews studies in which multilevel modelling was used.

A review of twenty papers that applied multilevel modelling techniques highlighted various differences and important findings. The most evident difference between the papers appeared to be the effect of contextual characteristics over and above compositional characteristics. Of the papers reviewed, six found that contextual characteristics (which included neighbourhood and regional characteristics) were associated with various measures of mental disorder, even after adjustment for compositional characteristics [118, 122, 132, 133, 138, 140]. However, it was found by Duncan et al. [141] that neighbourhood characteristics did not bear any importance for mental disorder, although they did find an effect of urbanicity, which they termed a regional difference. On the other hand, four found that contextual characteristics were not associated with the various measures of mental disorder in addition to compositional characteristics [120, 130, 135, 139]. These findings support the view that the evidence for the effect of place on mental health is inconsistent; however, it is important to realise that the studies were carried out on different populations, and so results may not be transferable from one population to another, especially as the size of the areas used varied between studies [142, 143]. The inconsistent evidence between studies regarding the importance of place has also led to differing opinions on policy implications. Wainwright and Surtees [137] argued that interventions may be better targeted at the individual rather than the area; however, both Driessen et al. [132] and Fone & Dunstan [140] argued that area-based interventions may be more suitable than interventions at the individual level.

Irrespective of the differences in conclusions across the different studies, it was found by most that, in general, any variation in measures of mental disorder between higher levels, such as postcode sectors, neighbourhoods and regions,

was very small. Instead, an important finding which emerged from the literature regarded variation at the household level. Several authors included household as a level in their analyses [120, 124, 139, 143], and all concluded that more variation occurred at the household level, as opposed to any levels above this, and that characteristics at the household level may be more important than characteristics of neighbourhood.

3.5 Objectives using Scottish Health Survey Data

A study by Stewart [30], carried out for a Masters dissertation, revealed that there was a shortage of information on risk factors for mental disorder in the Scottish population. By using data from the Scottish Health Survey (described in Section 2.2) as being representative of the population of Scotland, and using psychiatric admission as an indicator of poor mental health in Scotland, Stewart investigated various demographic, socioeconomic and lifestyle risk factors of psychiatric admission, and hence mental disorder in Scotland.

However, this study only employed single-level models, and, as discussed in Section 2.2, the Scottish Health Survey data was hierarchical in nature, with survey respondents nested within postcode sectors. Section 1.2 highlighted some potential problems with fitting single-level models to hierarchical data, such as underestimating standard errors. Therefore, work carried out in this thesis will seek to address these problems by fitting more sophisticated multilevel models to the SHeS dataset.

The study by Stewart found that there were significant differences in the likelihood of psychiatric admission between those who had never experienced a (known) psychiatric admission, and thus for whom any admission following survey interview would be a first admission, and those who had history of at least one previous psychiatric admission, and hence for whom any admission following survey interview would be a readmission. This suggested that risk factors for first admissions and readmissions should be considered separately. However, in the Scottish Health Survey dataset, the number of respondents with a history of previous admissions was small, and hence analyses in this thesis will

focus solely on first psychiatric admissions. Further discussion of this is given in Chapter 4.

To summarise, by using the GHQ-12 as an indicator of potential psychiatric morbidity, the objectives which will be addressed in the thesis using the Scottish Health Survey data are given below.

1. To investigate the association between the GHQ-12 and first psychiatric admission in Scotland.
2. To investigate if any association between the GHQ-12 and first psychiatric admission remains following adjustment for a range of individual- and area-level demographic, socioeconomic and lifestyle risk factors, and whether or not this is consistent with the reviewed literature.
3. To determine the 'best' threshold score for use of the GHQ-12 in Scotland.

4 Psychiatric Admissions in Scotland: Some Exploratory Analyses

This chapter gives an overview of the number of psychiatric admissions in the 1995 and 1998 Scottish Health Surveys as well as investigating the distribution of GHQ-12 score. Multilevel logistic regression models were fitted to provide some preliminary results for the objectives stated in Section 3.5. Results from these models are presented in Section 4.3.

4.1 Descriptive Statistics

4.1.1 Psychiatric Admissions in the Scottish Health Survey

Altogether 15 668 respondents to the two surveys gave permission for their data to be linked to the NHS administrative database enabling survey data to be linked with Scottish hospital records and death records from 1981 to 2004. Table 4.1 below displays the percentages of respondents who experienced at least one psychiatric admission following survey interview.

Table 4.1 - Psychiatric admission following survey interview

	No Admission	≥1 Admission	Total
Frequency	15453	215	15668
Percent (%)	98.6	1.4	100

It can be observed from Table 4.1 that only a small percentage of respondents experienced at least one psychiatric admission following survey interview (1.4%). This small number may be the result of a greater tendency to treat individuals with mental disorders in the community rather than admit to psychiatric care; however, this will be discussed further in Chapter 6.

There may also be differences in the percentage admitted to psychiatric facilities between the 1995 and 1998 surveys. The follow-up time for those

interviewed in the 1995 survey was longer, perhaps implying that a greater percentage of admissions is to be expected. Table 4.2 investigates this.

Table 4.2 - Psychiatric admission following survey interview by survey year

	1995 Survey	1998 Survey	Total
No Admission			
Frequency	7246	8207	15453
Percent (%)	98.4	98.8	98.6
≥1 Admission			
Frequency	117	98	215
Percent (%)	1.6	1.2	1.4
Total			
Frequency	7363	8305	15668
Percent (%)	100	100	100

Table 4.2 shows that there was a slightly higher percentage of admissions during follow-up for those who were interviewed in 1995 than in 1998 (difference of 0.4%). This may be as expected as a result of the longer follow-up period for respondents of the 1995 survey. The difference could also be due to differences in the age distributions between the two surveys. Recall that the 1995 survey was restricted to those under 65 years, whereas the 1998 survey was restricted to those under 75 years. If younger individuals are at a greater risk of admission, then a higher percentage of admissions may again be expected in the 1995 survey.

Stewart [30] reported differences in the likelihood of psychiatric admission depending on whether or not an individual had experienced at least one previous psychiatric admission. Using single-level logistic regression on the 1995 and 1998 linked SHeS dataset, Stewart found that those with at least one previous psychiatric admission had highly significantly greater odds (OR = 30.3, 95% CI = (22.4, 41.0)) of being admitted to psychiatric facilities following survey interview than those with no known history of psychiatric admission prior to survey interview. This result suggests it may be sensible to stratify analyses according to whether or not a respondent has a known history of psychiatric admission. This will mean that risk factors for first psychiatric admission and for readmission can be investigated separately. Table 4.3 below shows the percentage of subjects admitted to psychiatric facilities by type of admission, i.e. first admission if the respondent had no known history of psychiatric

admission prior to survey interview or readmission if the respondent had at least one psychiatric admission prior to survey interview. To recap, the rows of the table correspond to admissions following survey interview, and the columns of the table correspond to admissions prior to survey interview.

Table 4.3 - Psychiatric admission following survey interview by number of prior admissions

	No Prior Admission	≥1 Prior Admission	Total
No Admission			
Frequency	15168	285	15453
Percent (%)	99.1	78.5	98.6
≥1 Admission			
Frequency	137	78	215
Percent (%)	0.9	21.5	1.4
Total			
Frequency	15305	363	15668
Percent (%)	100	100	100

After omitting those with prior admission(s) there were 15305 respondents with no known history of psychiatric admission prior to survey interview, and of them only a small percentage was admitted to psychiatric facilities following survey interview (0.9%). Of the 363 respondents with history of at least one psychiatric admission prior to survey interview, 21.5% went on to be readmitted following survey interview. When considering first admissions and readmissions separately, Table 4.3 also reveals that the number of respondents who had at least one psychiatric admission prior to survey interview is very small (= 363). This is only 2.3% of the original 15668 respondents for whom data were available. Because of this small number of respondents, analyses will focus solely on investigating the association between GHQ-12 score and psychiatric admission for those with no known history of psychiatric admission prior to survey interview (i.e. respondents for whom any admission following survey interview is assumed to be a first-ever admission).

4.1.2 Distribution of GHQ-12 Score in the Scottish Health Survey

Each respondent in the SHeS had data recorded on actual GHQ-12 score (i.e. an integer-valued score between 0 and 12). However, rather than use the ordinal

version, GHQ-12 score was categorised into four categories corresponding to whether the respondent had a score of 0, 1-2, 3-4 or 5-12. Categories were defined in this way in order to distinguish between those with no or low risk of psychiatric caseness (i.e. a score of 0), those with a borderline risk of psychiatric caseness (i.e. a score of 1-2 or 3-4 depending on the threshold score employed) and those with a high risk of psychiatric caseness (i.e. a score of 5-12). Table 4.4 displays the distribution of GHQ-12 score in the SHeS.

Table 4.4 - Distribution of GHQ-12 score in SHeS

	Score 0	Score 1-2	Score 3-4	Score 5-12	Total
Frequency	8771	3232	1331	1971	15305
Percent (%)	57.3	21.1	8.7	12.9	100

The majority of respondents in the SHeS had a GHQ-12 score of 0 (57.3%), and would therefore be considered as being at low risk of psychiatric caseness, which, using these data, is being represented by having no admission to psychiatric facilities. Only 12.9% of respondents obtained a GHQ-12 score in the high risk category (a score of 5-12).

It is also of interest to check for any trend in the percentage of respondents admitted to psychiatric facilities across GHQ-12 score in order to informally investigate the association between GHQ-12 score and psychiatric admission, which is the primary objective using the SHeS data.

Table 4.5 - Psychiatric admission following survey interview by GHQ-12 score

	Score 0	Score 1-2	Score 3-4	Score 5-12	Total
No Admission					
Frequency	8725	3198	1313	1932	15168
Percent (%)	99.5	98.9	98.6	98.0	99.1
≥1 Admission					
Frequency	46	34	18	39	137
Percent (%)	0.5	1.1	1.4	2.0	0.9
Total					
Frequency	8771	3232	1331	1971	15305
Percent (%)	100	100	100	100	100

Table 4.5 demonstrates that, informally, psychiatric admission following survey interview appears to be associated with GHQ-12 score. The percentage of

respondents experiencing at least one psychiatric admission following survey interview increased as GHQ-12 score increased, indicating a possible increasing trend. This trend will be investigated formally in Section 4.3 of this chapter and in later chapters.

4.1.3 Missing Data in the Scottish Health Survey

Of the 15305 individuals with no known of history psychiatric admission prior to survey interview, 1584 (10.3%) had missing data on at least one variable. Two primary consequences of ignoring missing data include loss of power and biased estimates of associations [144]. Although the proportion of missing data in the SHeS was small, it was still of interest to impute values for the missing data since it is known that, even when the proportion of missing data is small, potential bias can still occur [145, 146].

Missing data were imputed in SPSS 14.0 [147] using the missing value analysis regression technique. This method involved treating variables with missing values as dependent variables to be predicted by the other variables in the dataset using multiple linear regression. As this produced continuous estimates for the imputed values, the imputed values obtained for categorical variables were rounded to the nearest whole category. It is accepted that other more sophisticated methods of imputation are available for this purpose, and these will be considered in the Discussion (Chapter 10). However, as the purpose of this thesis was not focused on estimating missing values, and also due to time constraints, only the multiple regression method described here was used.

When imputing missing data in SPSS using the missing value analysis regression technique, a random component can be added to the regression estimates to reflect the uncertainty associated with the imputation [148]. The random component selected can either be residuals, normal variates or Student's *t* variates. Alternatively, no adjustment can be made.

4.2 Applying Multilevel Modelling to Logistic Regression

In health research, it is common to observe outcomes that are not measured on a continuous scale. For example, some health outcome data are qualitative, and in particular binary. In that case there are two possible outcomes (of which only one can occur), such as ‘alive/dead’ or ‘pass/fail’. In general, these can be referred to as ‘response’ or ‘non-response’ depending on the outcome of interest.

Linear regression cannot be used sensibly to model these outcomes on a set of explanatory variables. Instead, so-called generalised linear models are applied in which there exists a linear predictor based on the explanatory variables

$$\eta = \sum x_p \beta_p ,$$

where the coefficients β_1, \dots, β_q are unknown.

In the case of binary data, the objective is to measure the response probability, π , based on a set of explanatory variables. A suitable link function, g , maps the response onto the predictor such that

$$g(\pi_i) = \eta_i = \sum x_{ip} \beta_p ,$$

for the i th unit ($i = 1, \dots, n$). There are a number of link functions available to do this. Only the logit/logistic function will be discussed here; however, a full discussion of other possible link functions is given in McCullagh and Nelder [149]. The logit/logistic function is of the form

$$g(\pi) = \log[\pi/(1-\pi)] = \text{logit}(\pi).$$

The logit link function allows values of $g(\pi)$, or $\text{logit}(\pi)$, to take any value in the range $(-\infty, \infty)$ by transforming the original probability values which are bounded between 0 and 1, whilst ensuring that predicted probabilities derived from the fitted model are in the range $[0,1]$ [150]. Some reasons why the logit/logistic function is favoured over alternative link functions are that it has simpler

theoretical properties and the coefficients from a logit model can be interpreted simply as logarithms of odds ratios (or as odds ratios when exponentiated) [149].

For a single-level logistic regression model, y_i denotes the binary response for the i th unit. The observed responses are proportions and follow a binomial distribution such that

$$y_i \sim \text{Bin}(1, \pi_i) ,$$

where π_i is the expected proportion for the i th unit. This is also referred to as a Bernoulli distribution. The probability of response, i.e. that $y_i = 1$, is denoted by π_i . The single-level logit model can then be written as

$$\text{logit}(\pi_i) = \beta_0 + \sum \beta_p x_{pi} ,$$

where x_{pi} ($p = 1, \dots, q$) is the row vector of explanatory variables for the i th level-1 unit. As discussed previously, the coefficient, β_p , from this model is interpreted as the change in the log odds ratio of a positive response relative to a negative response for each unit increase in the associated explanatory variable if the explanatory is continuous; or as the log odds ratio in the case of a categorical explanatory, where one level of the variable is selected as the baseline. Exponentiating the right-hand side of this model allows the coefficients to be interpreted as the odds ratio of a positive response relative to a negative response for each unit increase in the continuous explanatory variable, or as the odds ratio when the explanatory is categorical. Rearranging the model allows the probability of a positive response to be given as

$$\pi_i = \exp(\beta_0 + \sum \beta_p x_{pi}) / [1 + \exp(\beta_0 + \sum \beta_p x_{pi})] .$$

The single-level logistic regression model may be extended to a multilevel model with two or more levels in order to account for the clustering of binomial (binary) data nested within higher-level units. The response is given a further subscript, j , so that y_{ij} is the binary response for the i th individual nested within the j th unit ($j = 1, \dots, m$). Hence, the probability of response i.e. that $y_{ij} = 1$, is now denoted by π_{ij} .

Following the same form as the single-level model using the logit function, the multilevel logistic regression model is given as

$$\text{logit}(\pi_{ij}) = \log[\pi_{ij}/(1 - \pi_{ij})] = \beta_0 + \sum \beta_p x_{pij} + u_j.$$

As usual, the β_p are the coefficients for the fixed effects, x_{pij} ; however, in multilevel random intercept models, the intercept is allowed to vary randomly across the higher-level unit. u_j is the random effect of the higher-level unit. These higher-level residuals are assumed to follow a Normal distribution with mean 0 and variance σ_u^2 . The full model for estimating probabilities is then given as

$$\pi_{ij} = \exp(\beta_0 + \sum \beta_p x_{pij} + u_j) / [1 + \exp(\beta_0 + \sum \beta_p x_{pij} + u_j)].$$

The coefficients of the explanatory variables are interpreted in the same manner as in the single-level model. The significance of the fixed effects may be tested using Wald tests in MLwiN. Testing random parameters, i.e. σ_u^2 , is more difficult; however, a Wald test can provide an approximation. Snijders and Bosker [151] provide explanations of alternative methods for testing the random intercept.

When multilevel logistic regression is used, it is also possible to estimate the intraclass correlation (ICC). Goldstein et al. [152] discussed a number of procedures for calculating the ICC for discrete response models. In some cases, they may lead to different answers. In this thesis, all estimates of the ICC for the logistic regression models in Section 4.3 of this chapter have been calculated using a procedure called the ‘latent variable approach’ [152]. In this case, the ICC is estimated as

$$\text{ICC} = \sigma_u^2 / [\sigma_u^2 + \pi^2/3],$$

where π corresponds to the number π . For a number of examples to which multilevel logistic regression could be applied refer to Chapter 3 by Rice on Binomial Regression in Leyland & Goldstein [153].

4.3 Results from Multilevel Logistic Regression

As discussed in Section 3.5, the primary objective was to investigate the association between psychological distress, as measured by the GHQ-12, and first psychiatric hospital admission in Scotland using data from the Scottish Health Survey, while controlling for a range of risk factors. This section presents results obtained from fitting multilevel logistic regression models in MLwiN. Multilevel models were fitted in order to account for the hierarchical structure of the data which consisted of two levels - individuals nested within postcode sectors. The binary response was of the form 'subject did or did not experience a psychiatric admission following survey interview'. Results presented in this section are for those respondents with no psychiatric admissions prior to survey interview (see Section 4.1 for a further discussion of this). Results from the multilevel logistic regression models will give a prior insight into results to be expected from fitting the more complex multilevel event history models.

A binomial model with logit link was fitted to the imputed dataset including the random component (residual), and the parameter estimates were obtained using first-order penalised quasi-likelihood (PQL) estimation (see Section 5.3.5 for a discussion of estimation procedures). First-order PQL was used as parameter estimates would not converge when 2nd-order PQL was used. The outcome was assumed to be binomially distributed.

In Section 4.1, Table 4.5 showed that, subjectively, there appeared to be an increase in the percentage of respondents admitted to psychiatric facilities following survey interview as GHQ-12 score increased. To investigate if this increase was significant model A1, containing GHQ-12 score and a random intercept for postcode sector, was fitted.

Following the fitting of only GHQ-12 score in model A1, it was then of interest to investigate if the association between increasing GHQ-12 score and increased odds of psychiatric admission remained after adjustment for a range of individual- and area-level demographic, socioeconomic and lifestyle risk factors. As discussed in Section 3.2.1.2, GHQ-12 score is highly correlated with self-assessed general health in predicting mental health outcomes. Therefore, in

order to avoid potential over-controlling if both of these variables were included in the model, models were fitted both including and excluding self-assessed general health. Model A2 fitted all individual- and area-level risk factors apart from self-assessed general health, and finally, model A3 was fitted as in model A2 but including self-assessed general health. In order to investigate how much of the variation in the odds of psychiatric admission between postcode sectors could be explained by individual characteristics, models A2 and A3 were at first fitted allowing only for the adjustment of individual-level risk factors. After removal of all non-significant individual-level risk factors, area-level risk factors (which included a measure of deprivation and a measure of urbanicity) were added to the models. The remaining variation in the odds of psychiatric admission between postcode sectors explained by adding these variables could then be calculated.

Both estimates of the fixed and random parameters and estimated standard errors obtained from fitting the three separate models are presented in Table 4.6 below. Due to the large number of variables that were available in this dataset, Table 4.6 displays results for significant individual- and area-level risk factors only. Table 2.1 provides a comprehensive list of all available risk factors.

Results from model A1 demonstrated that there was a highly significant increasing trend in the odds of first psychiatric admission during follow-up as GHQ-12 score increased. It can also be observed that the odds of psychiatric admission for each category of GHQ-12 score were significantly different from that of the baseline score of 0. This indicated that any GHQ-12 score of 1 or more is significantly associated with psychiatric admission, implying that a score of 1 may be a suitable threshold score for the GHQ-12 in the Scottish population. After adjustment for GHQ-12 score, the probability of psychiatric admission in the average area for an individual with a GHQ-12 score of 0, obtained by taking the antilogit function of the intercept, was 0.0052. The intra-class correlation (ICC) indicated that 7.9% of the total variation was due to differences between postcode sectors.

Table 4.6 - Results from multilevel logistic regression

	Model A1 Estimate(s.e)	Model A2 Estimate(s.e)	Model A3 Estimate(s.e)
Fixed			
Intercept (β_0)	-5.253(0.150)	-5.731(0.310)	-5.940(0.327)
GHQ-12 Score			
0	0.000**	0.000**	0.000*
1-2 (β_1)	0.701(0.227)	0.580(0.229)	0.485(0.231)
3-4 (β_2)	0.959(0.280)	0.670(0.285)	0.512(0.290)
5-12 (β_3)	1.342(0.220)	0.930(0.229)	0.671(0.239)
Sex			
Male		0.000	0.000
Female (β_4)		-0.137(0.189)	-0.088(0.190)
Age			
16-24		0.000	0.000
25-34 (β_5)		-0.287(0.289)	-0.254(0.291)
35-44 (β_6)		-0.012(0.280)	0.028(0.283)
45-54 (β_7)		-0.682(0.336)	-0.737(0.339)
55-64 (β_8)		-0.277(0.307)	-0.397(0.312)
65-74 (β_9)		-0.112(0.387)	-0.082(0.389)
Marital Status			
Married/cohabiting		0.000	0.000
Other (β_{10})		0.534(0.180)	0.439(0.183)
Receipts of Benefits			
No		0.000	0.000
Yes (β_{11})		0.781(0.202)	0.567(0.211)
Smoking Status			
Non-Smoker		0.000	0.000
Current Smoker (β_{12})		0.794(0.215)	0.697(0.217)
Ex-Smoker (β_{13})		0.028(0.302)	-0.002(0.303)
Employment Status			
Full-Time		0.000	0.000
Unemployed (β_{14})		0.445(0.267)	0.573(0.272)
Part-Time (β_{15})		-0.353(0.255)	-0.303(0.256)
Self-Assessed Health			
Very Good			0.000
Good (β_{16})			0.566(0.226)
Fair (β_{17})			1.040(0.252)
Bad (β_{18})			0.319(0.558)
Very Bad (β_{19})			2.076(0.472)
Random			
Area Variation(σ_u^2)	0.281(0.268)	0.220(0.257)	0.239(0.255)
ICC	0.079	0.063	0.068

* $p_{\text{trend}} < 0.05$ ** $p_{\text{trend}} < 0.001$

Model A2 displays results obtained following adjustment for all significant individual-level risk factors excluding self-assessed general health. The increasing trend in the odds of psychiatric admission remained highly significant, and, in addition to having a GHQ-12 score of 1 or more, other significant risk factors associated with an increased odds of psychiatric admission included not being married (i.e. single, separated, divorced or widowed), being in receipt of benefits and finally, being a current smoker. Again this indicated that, even following adjustment for a range of other risk factors, a score of 1 appears to be a suitable threshold score for the GHQ-12 in the Scottish population. The between-postcode sector variation ($\sigma_u^2 = 0.220$) was reduced from model A1 to model A2, with approximately 22% of the total unexplained variation between postcode sectors being explained as a result of adjusting for further individual-level risk factors. Neither of the area-level risk factors was significantly associated with the outcome in addition to the individual-level risk factors.

In fitting model A3, self-assessed general health was also allowed to be included as a potential risk factor. The increasing trend in the odds of outcome remained significant following adjustment for all significant individual-level risk factors, of which those associated with an increased odds of psychiatric admission, in addition to a GHQ-12 score of 1 or more, included the following: not being married (i.e. single, separated, divorced or widowed); being in receipt of benefits; being a current smoker; being unemployed; and having a self-assessed general health rating of other than 'very good'. As with the two previous models, this model demonstrated that, even after adjustment for a range of other risk factors, this time including self-assessed general health, a GHQ-12 score of 1 appeared to be an appropriate threshold score in the Scottish population. Again, neither of the area-level risk factors was associated with the outcome when added to the model including all the significant individual-level risk factors. The between-postcode sector variation in model A3 ($\sigma_u^2 = 0.239$) increased from model A2 as a result of including self-assessed general health. An explanation of this phenomenon can be found in Snijders and Bosker [151].

4.4 Chapter Summary

Fitting multilevel logistic regression models has given an insight into individual-level and area-level risk factors associated with first psychiatric admission in Scotland, while acknowledging the hierarchical structure of the data. However, as the data were from the 1995 and 1998 Scottish Health Surveys, the lengths of follow-up times from survey interview until 2004 were different for the two surveys. A more appropriate approach, which would account for differences in follow-up times between the two surveys, is to use multilevel event history models. One of the main differences in using event history analysis methodology over logistic regression is that time until the event of interest can be partially observed. In this case, for subjects who experience a psychiatric admission after survey interview, the time variable records the actual time to event. However, for subjects who do not experience a psychiatric admission, the time variable refers to length of follow-up. This is an incomplete observation of survival time, and these incomplete observations are referred to as being 'censored'. In this study, observations will be censored if the subject dies or reaches the end of follow up without experiencing a psychiatric admission (or if they are lost to follow-up). Event history models are particularly important when the length of follow-up is long, and therefore the number of individuals dying or being lost to follow-up may be large. Additionally, it has been shown in previous literature that psychological distress, as measured by the GHQ, is associated with a higher risk of mortality [154, 155]. Since results from the multilevel logistic regression in Table 4.6 showed that those with a higher GHQ score were at a greater risk of psychiatric admission, based on the previous literature this would also imply that individuals with an increased risk of psychiatric admission are at greater risk of death, and hence censoring. Once again this demonstrates that the use of multilevel event history models is preferred over multilevel logistic regression.

5 Multilevel Event History Modelling: A Review

5.1 Introduction

This chapter will provide a review of conventional methods used for fitting multilevel event history models to public health data. It will discuss problems which may be encountered when datasets are large, as is usually the case with public health survey data. Successive chapters review possible methods which could be used to overcome these problems.

Event history models are also commonly referred to as ‘survival models’ in the context of biology and health. Since this thesis is concerned with the application of event history models to public health research, such models will now be referred to as ‘survival models’ in the text.

5.2 Single-Level Survival Modelling

5.2.1 Introduction to Survival Modelling

When analysing medical or public health datasets, it may often be of interest to measure the time until a particular pre-defined event occurs, such as death from a particular disease. This time is known as the survival time. With the SHeS dataset, interest was in observing the time until first psychiatric hospital admission as measured from survey interview, and the effect that demographic, socioeconomic and lifestyle risk factors had on the survival time. If time until event, i.e. the survival time, is treated as a continuous variable, it may seem reasonable to regress the natural logarithm of time on the covariates; however, as discussed in Allison [156] and Petersen [157], there are two problems with this approach. Firstly, there may be some individuals who do not experience the event of interest during the period of follow-up. For example, when following-up individuals in the SHeS data to measure time until first psychiatric hospital admission, it is highly likely that not all individuals will experience a psychiatric hospital admission during the follow-up period. These individuals are referred to

as ‘right-censored’. Right-censoring implies that it is known only that the individual has not experienced the event of interest by the end of the follow-up period. Other types of censoring are ‘left-censoring’ and ‘interval-censoring’. These will not be considered here, but definitions can be found in Kalbfleisch & Prentice [158]. It is known that ignoring censoring can lead to large biases [156]. The second problem with modelling survival times using ordinary regression methods is that they cannot include time-varying covariates. Instead, survival models such as the proportional hazards model or accelerated lifetime model must be used in order to regress survival times on covariates of interest. Survival models account for censored observations and time-varying covariates, and therefore overcome the problems associated with using ordinary regression methods. This section gives a brief summary of survival analysis methodology in the case of single-level data. Section 5.3 will then describe how these methods can be extended to incorporate random effects in the case of multilevel data.

Survival models are applied when the outcomes are measures of duration. In general, the fundamental aim of survival analysis is to use the data to provide estimates of the probability of surviving beyond a specified time. This probability is known as the ‘survivor function’. If T is defined as a continuous non-negative random variable representing the failure time of an individual from a homogeneous population, then the survivor function is defined as

$$S(t) = P(T \geq t) = 1 - F(t),$$

where $0 < t < \infty$ and $F(t)$ is the cumulative distribution function.

It has been shown, however, that survival data are modelled more appropriately through the ‘hazard function’. The term ‘hazard’ is used to describe the concept of the risk of ‘failure’ in an interval after time t , conditional on the subject having survived to time t [1].

The hazard function (hazard rate) is defined as

$$h(t) = \lim_{\Delta \rightarrow 0} \{P(t \leq T < t + \Delta \mid T \geq t)\} / \Delta,$$

and specifies the instantaneous rate of failure. The hazard function can also be defined in terms of the survivor function so that

$$h(t) = f(t)/S(t),$$

where $f(t)$ is the probability density function.

The survivor and hazard functions may be estimated parametrically by fitting any non-negative distribution to describe the survival data. They may also be estimated non-parametrically, for example, using the Kaplan-Meier estimator. The most common parametric distributions for describing survival data include the exponential, Weibull, log-normal, gamma and so on. These will not be discussed in detail here; however, a review of the most commonly used parametric distributions can be found in books by Cox & Oakes [159], Klein & Moeschberger [160], Hougaard [161] and Kalbfleisch and Prentice [158]. Choice of parametric distribution depends on a number of different factors, for example, the type of survival data (e.g. human lifetimes) and their convenience for statistical inference. Cox & Oakes [159] and Hougaard [161] provide comparisons of parametric distributions used for describing survival data based on, among others, properties of the hazard and the number of parameters in the distribution. However, as discussed above, it is possible to avoid assuming a particular parametric distribution altogether by using non-parametric methods. Common non-parametric methods for estimating the survivor function in the presence of right-censoring include the Kaplan-Meier estimator, also known as the Product-Limit estimator, and the Nelson-Aalen estimator. Again, these will not be covered here, but full definitions of these estimators can be found in Hougaard [161] and Kalbfleisch & Prentice [158]. A clear disadvantage of the non-parametric methods is that estimation of the hazard function is not possible therefore, if interest lies more in estimating the hazard function rather than the survivor function, parametric methods should be used. For further comparisons of parametric and non-parametric methods refer to Hougaard [161].

With survival data, there may also be information available on a number of explanatory variables or covariates, which may have an effect on failure time. The most commonly used models are the proportional hazards and accelerated lifetime models. Both will now be considered.

5.2.2 Proportional Hazards Model

If $h(t, x)$ is the hazard function at time t for an individual with covariate vector x , then the proportional hazards model (PHM) is defined as

$$h(t; x) = h_0(t) \exp(\beta^T x) ,$$

Equation 5.1

where $h_0(t)$ is a baseline hazard function (i.e. the hazard for an individual with $x=0$), and β is a vector of unknown regression parameters. The survivor function is thus given as

$$S(t; x) = P(T > t | x) = [S_0(t)]^{\exp(\beta^T x)} ,$$

where $S_0(t)$ is the baseline survivor function, and can be written in terms of the baseline hazard function, $h_0(t)$, as follows:

$$S_0(t) = \exp\left\{- \int_0^t h_0(u) du\right\} .$$

The baseline hazard function, $h_0(t)$, could assume some parametric form. More commonly, however, the form of the baseline hazard is left unspecified yielding the widely-used semi-parametric (Cox) PHM. This model is semi-parametric in the sense that a parametric form is assumed only for the covariate effect, with the baseline hazard function treated non-parametrically. When the model is semi-parametric, the method of analysis for estimation of the β regression parameters is partial likelihood, with the hazard function being treated as a nuisance parameter. If it is assumed that censoring is non-informative right-censoring, this method is based on the conditional probability that individual i experiences the event in the next unit of time, $t_i + \delta t_i$, given that only one individual from the risk set (R_i , i.e. the set of individuals at risk at time t_i) fails at that time.

Therefore, supposing that there are no tied observations, under the PHM this conditional probability can be written as

$$\frac{h_0(t)\exp(\beta^T x_i)}{\sum_{j \in R_i} h_0(t)\exp(\beta^T x_j)} .$$

This expression simplifies since the baseline hazard function, $h_0(t)$, cancels out, therefore, the partial likelihood for β is

$$L(\beta) = \prod_{i=1}^m \left[\frac{\exp(\beta^T x_i)}{\sum_{j \in R_i} \exp(\beta^T x_j)} \right] .$$

for m distinct failure times. There are various ways in which the partial likelihood can be modified when there are tied observations among the uncensored failure times. These will not be considered here, but a full explanation can be found in Klein & Moeschberger [160] and Kalbfleisch and Prentice [158].

Although the β regression parameters may be estimated using the partial likelihood as described above, it may also be of interest to estimate the survivor function for any set of values of the covariates. There are a number of ways this can be done non-parametrically, and, although they will not be covered here, a review can be found in Kalbfleisch & Prentice [158].

In some cases, there may be information on covariates whose values change over the course of the study, i.e. time-varying covariates. The PHM can easily be extended to incorporate time-varying covariates. Information on this can be found in Klein & Moeschberger [160].

5.2.3 Accelerated Lifetime Model

Although perhaps not as widely used as the proportional hazards model, the accelerated lifetime model is, however, another commonly used model in survival regression analysis. The hazard function for duration in the accelerated lifetime model is defined as

$$h(t; \mathbf{x}) = h_0\{t \exp(\beta^T \mathbf{x})\} \exp(\beta^T \mathbf{x}) ,$$

Equation 5.2

where h_0 is the baseline function, and \mathbf{x} is the covariate vector. From this it is clear that the explanatory variables have a direct effect on the survival time, and accelerate or decelerate the time to failure [162]. This effect makes interpretation of results clearer in the accelerated lifetime model, where results refer to the effect of covariates on the mean survival time; rather than in the PHM, where instead results refer to the effects of covariates on a conditional probability [162]. As well as the fact that interpretation of results is generally simpler using the accelerated lifetime model, another reason why it may be preferred over the PHM is that it does not require the assumption of proportional hazards. Instead, the accelerated lifetime model assumes proportional probability of the survival time and the baseline survival i.e. $P(T > t \mid \mathbf{x}) = P(t_0 > t \exp(\beta^T \mathbf{x}))$ [163].

The above function can be written as a log linear model for the random variable T , modelling the relationship between the (natural) logarithm of survival time and the covariates such that

$$\ln(T) = \alpha + \beta^T \mathbf{x} + \sigma \varepsilon ,$$

where α is the intercept and estimate of overall median survival time on the natural log scale [163], \mathbf{x} is the vector of covariates, β is a vector of unknown regression parameters, σ is an unknown scale parameter, and ε is the random error term [164] with mean zero and a distribution not depending on \mathbf{x} [159]. Examples of distributions for the random error term include the Normal,

Extreme value, Logistic or Gamma distribution. Skron dal & Rabe-Hesketh [165] discussed examples of accelerated lifetime models depending on the distribution for the error term - the log-normal duration model if ε is Normally distributed; the log-logistic duration model for a logistic ε ; and the Weibull duration model if ε follows an extreme value (Gumbel) distribution. The accelerated lifetime model and proportional hazards model are indeed connected if the extreme value distribution is used [166] in that the Weibull duration model possesses both the proportional hazards and accelerated lifetime properties [165]. If the distribution of the error term is left unspecified, the accelerated lifetime model may be considered as a semiparametric alternative to the Cox model [158].

Maximum likelihood can be used to estimate the accelerated lifetime model. Estimation procedures for the accelerated lifetime model will not be considered here; however, Kalbfleisch & Prentice [158] considered use of the censored data rank test for estimating the β regression parameters.

As in the proportional hazards model, time-varying covariates may also be incorporated into the accelerated lifetime model. Information on the inclusion of time-varying covariates in the accelerated lifetime model can be found in Cox & Oakes [159] and Kalbfleisch & Prentice [158].

5.3 Multilevel Survival Modelling

5.3.1 Extending the Single-Level Model

This section will briefly describe how single-level survival models may be extended to incorporate random effects, in particular with reference to the PHM and accelerated lifetime model. Further details of how these multilevel models may be fitted using appropriate software is given in Sections 5.3.3 and 5.3.4.

The single-level proportional hazards and accelerated lifetime models may be extended to incorporate a multilevel structure. As discussed by Goldstein [166], the multilevel structure of a survival model may arise in two ways. The first corresponds to when there are repeated durations within individuals, and the

second corresponds to when each individual has a single duration, but the individuals are grouped within higher-level units. With the SHeS data, interest lies only in measuring the time until first ever psychiatric admission of individuals who are nested within postcode-sectors. Therefore, the multilevel structure when fitting survival models to the SHeS data is a single duration for each individual with individuals grouped within higher-level units.

Suppose individuals are nested within higher-level units. Then the 2-level proportional hazards model for the ij th level-1 unit is

$$h(t_{ij}; \mathbf{x}_{ij}) = h_0(t_{ij})\exp(\beta^T \mathbf{x}_{ij}) .$$

Similarly, the 2-level accelerated lifetime model for the ij th level-1 unit is

$$h_{ij}(t) = h_0\{t\exp(\beta^T \mathbf{x}_{ij})\}\exp(\beta^T \mathbf{x}_{ij}) .$$

In the above models, t is a continuous variable, h_0 is the baseline hazard function and \mathbf{x}_{ij} is the column vector of explanatory variables for the level-1 units. Explanatory variables may be defined at any level and, as with the single-level PHM, time-varying covariates, i.e. covariates that vary across failure times, may be included in the multilevel model. The multilevel PHM and accelerated lifetime model may be extended to include any number of random effects.

5.3.2 Software for Fitting Multilevel Models

Kelly [167] provided a comprehensive review of six computer packages which may be used for analysing correlated survival data, namely, SAS, Stata, S-Plus, R, MLwiN and WinBUGS. In terms of using these packages for fitting multilevel survival models, the author reviewed them on the basis of the estimation method used, distributions available for the random effect and user-friendliness. It was concluded that MLwiN and WinBUGS were the most suitable packages for fitting survival models with more than one random effect, with MLwiN being the most suitable when fitting a model to a hierarchical structure and WinBUGS being preferable if modelling a complex structure. The rest of this chapter

considers the use of MLwiN for fitting multilevel survival models and in particular, its suitability for fitting multilevel survival models to large datasets. The use of WinBUGS for fitting such models is considered in Chapter 7.

MLwiN is a package specially designed for fitting multilevel models. The latest version is MLwiN 2.16, which may be downloaded from <http://www.cmm.bristol.ac.uk/MLwiN/index.shtml>. Academics in the UK may download MLwiN for free.

Although fitting multilevel survival models is not a standard feature of MLwiN, macros for fitting both the accelerated lifetime and proportional hazards models are available from the MLwiN website stated above. The use of these macros is considered in Sections 5.3.3 and 5.3.4. The estimation procedures used in MLwiN are discussed in Section 5.3.5. A manual for modelling survival data in MLwiN version 1.20 was written by Yang & Goldstein [163]. This manual is also appropriate for higher versions of MLwiN.

5.3.3 Fitting a Multilevel Proportional Hazards Model in MLwiN

5.3.3.1 Fitting a Multilevel Poisson Model

Both proportional hazards models and accelerated lifetime models (referred to in MLwiN as a ‘log-duration’ model) can be fitted in MLwiN. This section provides an overview of how multilevel proportional hazards models can be fitted in MLwiN. A guide to fitting accelerated lifetime models is provided in Section 5.3.4.

Yang & Goldstein [163] detailed briefly how the multilevel proportional hazards model for the ij th individual may be fitted in MLwiN using a Poisson model with log link as follows:

$$y_{gij} = \ln(d_{gij}) \approx \ln(n_{gij}) + \ln[(t_{g+\Delta} - t_g)h_0(t_g)] + \beta^T x_{ij} ,$$

which may be rewritten as

$$y_{gij} = \ln(d_{gij}) \approx (\text{offset}) + \varphi(t_g) + \beta^T x_{ij} ,$$

Equation 5.3

where $\varphi(t_g)$ is a function of time used to model the baseline hazard function. Possible forms for $\varphi(t_g)$ will be discussed in Section 5.3.3.3. The offset is the natural logarithm of the number of tied observations, n_g . This section gives a slightly more detailed account of how these expressions are obtained.

Recall from Equation 5.1 that the proportional hazards model at time t for individual with covariate x is expressed as

$$h(t; x) = h_0(t) \exp(\beta^T x) ,$$

and that the β regression parameters are estimated using the partial likelihood

$$L(\beta) = \prod_{i=1}^m \left[\frac{\exp(\beta^T x_i)}{\sum_{j \in R_i} \exp(\beta^T x_j)} \right] .$$

Equation 5.4

Suppose, for each time t_g ($g = 1, \dots, h$), Y_g are independent Poisson random variables with mean μ_g , where

$$\mu_g = m_g \exp(a_g + \beta^T x)$$

where m_g is the total number of individuals at time t_g and $\exp(a_g) = (t_{g+\Delta^-} - t_g)h_0(t_g)$.

For each individual in the risk set at time t_g , an artificial Poisson response is defined such that

$$d_{gi} = \begin{cases} 1 & \text{if } i \text{ fails at } t_g \\ 0 & \text{otherwise} \end{cases} .$$

Whitehead [168] showed that, when all failure times are distinct, i.e. $d_{gi} = 1$ at t_g for one individual only and 0 for the rest, the likelihood of the Poisson model at its maximum is proportional to the maximum of the likelihood in Equation 5.4. This demonstrates that the estimates of β are identical for the Poisson and proportional hazards models. Whitehead then went on to describe how the Poisson model can incorporate tied observations by setting $Y_g = n_g$, where n_g is the number of failures at t_g (i.e. $n_g = \sum_i d_{gi}$), and showed how the likelihood for this Poisson model at its maximum is proportional to the likelihood for β in Peto's generalisation of the proportional hazards model to incorporate ties. This proves that this Poisson model and Peto's survival model obtain identical estimates of β .

Now, it was described by McCullagh & Nelder [149] that because of the equivalence between the multinomial and Poisson likelihoods, the estimates of β obtained from the Poisson and multinomial likelihoods are also identical. Thus, based on the above, the estimate of β obtained from the multinomial likelihood is identical to that from the partial likelihood for β in Equation 5.4. McCullagh & Nelder then described that to adjust for tied observations in the multinomial log likelihood using Peto's method, the multinomial total should be set to equal the number of ties at that time (n_g , say). This implies that the Poisson log likelihood is equivalent to Peto's version of the partial likelihood. Following McCullagh & Nelder, when adjusting for tied observations, the 'probabilities' of the multinomial response model become

$$n_{gij} \pi_{gij} = \frac{n_{gij} \exp(\beta^T x_{ij})}{\sum_j \exp(\beta^T x_{ij})} ,$$

and therefore the equivalent log-linear model becomes

$$\log(\mu_{gij}) = \log[n_{gij}\exp(a + \beta^T x_{ij})]$$

i.e.

$$\begin{aligned}\log(\mu_{gij}) &= \log[n_{gij}\exp(a)\exp(\beta^T x_{ij})] \\ &= \log[n_{gij}(t_{g+\Delta}-t_g)h_0(t_g) \exp(\beta^T x_{ij})] \\ &= \log(n_{gij}) + \log[(t_{g+\Delta}-t_g)h_0(t_g)] + \beta^T x_{ij} .\end{aligned}$$

This is equivalent to Equation 5.3.

For the multilevel proportional hazards model, Ma et al. [169] showed how random effects Poisson models can be used to estimate random effects (Cox) proportional hazards models. A variance components model for the expected Poisson count is

$$\pi_{ij} = \exp(\alpha_g + \beta^T x_{ij} + u_j) ,$$

where α_g estimates the baseline hazard function which will be described in Section 5.3.3.3.

From Equation 5.3, it can be observed that, in order to fit Poisson models, each duration is expanded so that every individual has a series of records - one for each time point until either the event of interest or censoring occurs. This expansion allows the variable d_g to be created, where d_g is a count of the total number of failures at time t_g . Recall also that the ij th individual will have a value $d_{gij}=0$ for each time point they survive, with this becoming $d_{gij}=1$ if the individual experiences the event of interest. Therefore, counting up each of the $d_{gij}=1$ at a particular time point will give the total number of failures at that time. This expanded dataset is referred to as a person-period dataset, and will be discussed further in Section 5.3.3.2.

5.3.3.2 Obtaining the Person-Period Dataset

Section 5.3.3.1 noted that, in order to fit the Poisson model, a person-period dataset must first be created. This requires each individual's record to be replicated as many times as the observed number of time intervals until either the event of interest or censoring occurs. Clearly, this leads to an expansion in the size of the original dataset. Using the Scottish Health Survey dataset, this section will demonstrate how the person-period dataset required to fit the Poisson model is created in MLwiN.

To fit the Poisson model, MLwiN requires the person-period dataset to include the following five columns: the response for each individual, d_{gij} ; the number of total failures, d_g , at each time t_g ; a risk time indicator, i.e. an indicator of the risk set corresponding to each event time; a column of the survival (event) times and, finally, the number of individuals at the start point of the time. The 'SURV' command in MLwiN performs the data expansion to create the expanded dataset containing the five columns as well as information on available covariates. The process for expansion of the Scottish Health Survey dataset will now be considered.

As discussed previously, the dataset is rearranged so that every individual has a line of data corresponding to each time, t_g , until failure or censoring occurs. Because time is treated as a continuous variable, each t_g corresponds to each distinct event time. Section 4.1.1 noted that, in the SHeS dataset, 137 individuals experienced the event of interest, i.e. admission to psychiatric facilities. This implies that there should be 137 event times; however, as two individuals were admitted at the same number of days from survey interview, there were only 136 distinct event times. Consequently, there were also 136 risk sets, since a risk set was defined for each distinct failure time, t_g .

Consider the SHeS data for the first few individuals in the first postcode sector, shown below in Table 5.1. Note that, for illustrative purposes, Table 5.1 below only includes covariate information on GHQ-12 score.

Table 5.1 - Sample of SHeS Data before Expansion

Postcode Sector	Level-1 ID	GHQ-12 Score	Survival Time	Censoring Indicator (1=censored)
1	1	1-2	3277	1
1	2	3-4	3309	1
1	3	5-12	3315	1
.
.
.

Following the data expansion, obtained via the ‘SURV’ command in MLwiN, the person-period dataset for individual 1 in postcode-sector 1 now appears as in Table 5.2 below.

Table 5.2 - Sample of SHeS Data after Expansion

Postcode Sector	Level-1 ID	GHQ-12 Score	Response	Failure	Risk-Time Indicator	Survival Time	Number at Risk
1	1	1-2	0	1	1	20	15301
1	1	1-2	0	1	2	40	15297
1	1	1-2	0	1	3	44	15296
1	1	1-2	0	1	4	51	15291
1	1	1-2	0	1	5	63	15288
1	1	1-2	0	2	6	65	15285
.
.
1	1	1-2	0	1	135	2943	6825
1	1	1-2	0	1	136	3046	5023

Table 5.2 above contains the five columns created by the ‘SURV’ command in MLwiN and also any covariate information. The ‘response’ column corresponds to d_{gij} and, therefore, takes the value 0 for each time point the individual survives and the value 1 if the individual experiences the event of interest. If and when a value of 1 is observed, data collection terminates for this individual. The ‘response’ column is the only column from the five created by the ‘SURV’ command that is specific to a particular individual i.e. each individual has their own response vector, whereas the other four columns correspond to the whole dataset; therefore, the information in these four columns is replicated for each individual in the dataset.

From this table it can be observed that the first psychiatric admission (i.e. the first event) occurred at 20 days from survey interview. As time is being treated as a continuous variable, this distinct failure time is treated as a risk set. Hence, in this case, the failure at 20 days from survey interview was the first risk set as indicated by the ‘risk-time indicator’ column. It can be further observed that

there were 136 risk sets corresponding to each of the 136 distinct failure times. As discussed above, although there were 137 psychiatric admissions, there were only 136 distinct failure times since two individuals were admitted at the same number of days from survey interview. Table 5.2 shows that the ‘tied observation’ occurred in the 6th risk set which corresponds to a failure time of 65 days. Thus, two individuals were admitted to psychiatric facilities at 65 days as measured from the date of their respective survey interviews. Recall that tied observations are accounted for by the offset in the Poisson model, which is the logarithm of the number of failures at a particular time, t_g ; hence, in the 6th risk set, the offset would take the form $\log_e(2)$.

With respect to the first individual in the first postcode-sector, the expanded dataset shows that this individual did not experience the event of interest i.e. they were not admitted to psychiatric facilities at any time during follow-up. This is clear as the response vector for this individual contains only zeros. It should also be noted that this individual remained in the study until past the time of the last psychiatric admission (at which point they were censored). This is because they have a risk set corresponding to each of the 136 distinct failure times. If an individual is censored at any point during the study, either as a result of death or being lost to follow-up, data collection terminates for this individual; however, their response at time t_g of termination would be zero indicating that termination was a result of censoring and not a result of experiencing the event of interest.

Creation of the person-period dataset (Table 5.2) led to a vast expansion in the size of the original dataset (Table 5.1). The person-period dataset contains just below 1.9 million observations within individuals compared to the original dataset which contains 15305 individuals.

5.3.3.3 Modelling the Baseline Hazard Function

In Equation 5.3, $\varphi(t_g)$ denoted a function of time used to model the baseline hazard function. Possible forms for $\varphi(t_g)$ will now be considered. These may include fitting a polynomial function, using blocking factors, or assuming some

parametric form, such as the Weibull or Exponential distribution. Consider first the use of blocking factors.

Blocking factors are a set of dummy variables corresponding to the risk sets, and take the form

$$\alpha_1 Z_1 + \alpha_2 Z_2 + \dots + \alpha_l Z_l ,$$

where the α 's are parameters to be estimated and for $g = 1, \dots, l$;

$$Z_g = \begin{cases} 1 & \text{for } t_g \\ 0 & \text{otherwise} \end{cases}$$

There may be a dummy variable corresponding to each risk set. Alternatively, one risk set may be taken as the baseline with the dummy variables then corresponding to the difference in the baseline log hazard between every other risk set and the baseline risk set. This implies there will either be t_g or t_{g-1} dummy variables respectively. For the SHeS dataset, when time is being treated as a continuous variable, recall that there were 136 risk sets. Thus, if using blocking factors, there would either be 136 or 135 dummy variables. This is a large number of parameters to be estimated, and therefore this method is not recommended if there are a large number of risk sets [163]. Indeed, Goldstein [166] and Yang & Goldstein [163] discussed that, instead of adopting the blocking factors approach, fitting all of these nuisance parameters may be avoided by using a polynomial function to obtain efficient estimates of the model parameters. Yang & Goldstein also noted that the higher the order of the polynomial, the better the approximation to the baseline hazard and other estimates in the model. The polynomial function takes the form

$$\alpha_1 \log(t_g) + \alpha_2 [\log(t_g)]^2 + \dots + \alpha_l [\log(t_g)]^l .$$

The order of the polynomial should be experimented with until adding further terms does not alter the model parameters [163].

As discussed above, a parametric form may be assumed for the baseline hazard function. However, in this thesis, only semiparametric proportional hazards models will be fitted in MLwiN, and therefore parametric forms will not be considered here, although Yang & Goldstein [163] briefly described how the Weibull and Exponential distributions could be fitted in MLwiN to model the baseline hazard function.

5.3.3.4 Checking the Proportional Hazards Assumption

As implied by the name, the so-called ‘proportional hazards’ model requires the assumption of proportional hazards to hold, otherwise the model can lead to incorrect inferences [170]. The proportional hazards assumption states that the relative hazard for the i th individual is proportional in relation to any change of the covariates [163] i.e. that

$$\frac{h_i(t)}{h_0(t)} = \exp(\beta^T x_i) \quad .$$

In other words, the ratio of the hazard functions is constant with respect to time, and hence the hazard functions $h_i(t)$ and $h_0(t)$ are assumed proportional [170]. There are a number of possible methods available for assessing the proportional hazards assumption. A comprehensive review of several methods can be found in Hess [170]. Yang & Goldstein [163] also described possible methods which can be used in MLwiN to check the assumption. The method termed ‘checking the relative hazards’ by Yang & Goldstein will be used for checking the assumption in this thesis. This method involves including a time-dependent variable by creating an interaction term between the variable of interest and the logarithm of time and treating it the same as other time-independent variables. A non-significant interaction implies that the proportional hazards assumption is satisfied.

5.3.4 Fitting a Multilevel Accelerated Lifetime Model in MLwiN

This section summarises how a multilevel accelerated lifetime model may be fitted in MLwiN. The notation follows that of Yang & Goldstein [163].

Recall from Equation 5.2 that the form of the general hazard function under the accelerated lifetime model for the i^{th} individual in the j^{th} level-2 unit at time t is

$$h_{ij}(t) = h_0\{t\exp(\beta^T x_{ij})\}\exp(\beta^T x_{ij}) .$$

Also, if t_0 is an event time from the baseline distribution (i.e. when the values of the covariates are zero), then, following a natural logarithm transformation, the accelerated lifetime model with the effects of covariates is

$$\log(T_{ij}) = a + \beta^T x_{ij} + u_j + \log(t_0) ,$$

which may be rewritten as

$$y_{ij} = a + \beta^T x_{ij} + u_j + e_{ij} ,$$

where u_j is the random effect for the j^{th} level-2 unit and follows a Normal distribution with mean zero and variance σ_u^2 . The exponential of the random effects measures the difference of median survival times among the level-2 units [163]. Recall that the term for the baseline survival time (t_0), e_{ij} , can be assumed to come from a number of different distributions as discussed in Section 5.2.3. Because the dependent variable, y_{ij} , is the (natural) logarithm of the survival time, this model is also referred to as the ‘log-duration’ model [163].

There are a set of macros, named ‘SURVIVAL-V2’, which are used to fit multilevel log-duration models in MLwiN. Although no data expansion is required to fit this model (as was required when fitting a proportional hazards model via a Poisson model), some data preparation is required in order to use the macros. A brief summary will be provided in this section, but full details can be found in Yang & Goldstein [163].

The macro requires a distribution to be specified for the error term, e_{ij} . MLwiN allows a choice of four distributions: Normal, Extreme value, Gamma, or Logistic. Another requirement is that information on the event should be contained in a column named 'UNCENS', taking the value 1 if the ij^{th} individual experienced the event of interest or 0 if the ij^{th} individual was censored.

5.3.5 Estimation of Parameters in MLwiN

In MLwiN, model parameters are estimated using iterative generalised least squares (IGLS). However, before this method may be applied for non-linear models like the Poisson model, discussed in Section 5.3.3.1, quasi-likelihood methods are used to approximate generalised linear multilevel models by linear multilevel models. Marginal quasi-likelihood (MQL) and penalised (or predictive) quasi-likelihood (PQL) are the types of approximation available in MLwiN. This section will discuss the IGLS algorithm, MQL and PQL as well as the advantages and disadvantages of using these two approximations. Notation will follow that of Goldstein [166, 171] and Goldstein & Rasbash [172].

5.3.5.1 Iterative Generalised Least Squares

Consider a linear variance components model with two levels and, for illustration purposes, just one explanatory variable,

$$y_{ij} = \beta_0 + \beta_1 x_{ij} + u_j + e_{ij} .$$

Suppose the residual covariance matrix, $V = \text{cov}(Y | BX)$, is known. Here, Y is the response vector and X is the design matrix for the explanatory variable(s), where X_{ij} is the ij^{th} row of X . Then the estimators for the fixed coefficients can be obtained using Generalised Least Squares (GLS)

$$\hat{\beta} = (X^T V^{-1} X)^{-1} X^T V^{-1} Y ,$$

Equation 5.5

and

$$\text{cov}(\hat{\beta}) = (X^T V^{-1} X)^{-1}.$$

It has been shown by Goldstein [171] that, when the residuals follow a Normal distribution, Equation 5.5 also generates maximum likelihood estimates. The iterative estimation procedure starts from reasonable estimates of the fixed parameters. These are usually obtained from an initial ordinary least squares (OLS) fit, where it is assumed that $\sigma_u^2 = 0$. Here, σ_u^2 is the variance at level-2. This yields the OLS estimates of the fixed coefficients, $\hat{\beta}_{(0)}$. From this, the ‘raw’ residuals are formed,

$$\tilde{y}_{ij} = y_{ij} - \hat{\beta}_0 - \hat{\beta}_1 x_{ij},$$

and the vector of raw residuals is written

$$\tilde{Y} = \{ \tilde{y}_{ij} \}.$$

V is then simply the expected value of the cross-product matrix $\tilde{Y} \tilde{Y}^T$, i.e.

$$V = E(\tilde{Y} \tilde{Y}^T) = E(Y^*), \text{ say.}$$

By stacking the columns of the cross-product matrix it can be rearranged into a vector, $\text{vec}(Y^*) = Y^{**}$, say. A linear model involving the random parameters can then be written as

$$E(Y^{**}) = Z^* \theta,$$

where Z^* is the design matrix for the random parameters. θ may then be estimated using GLS

$$\hat{\theta} = (Z^{*T} V^{*-1} Z^*)^{-1} Z^{*T} V^{*-1} Y^{**},$$

Equation 5.6

where

$$V^* = V \otimes V .$$

Here, \otimes is the Kronecker product. The covariance matrix of $\hat{\theta}$ is given as

$$\text{cov}(\hat{\theta}) = (Z^{*\text{T}}V^{*-1}Z^*)^{-1}Z^{*\text{T}}V^{*-1}\text{cov}(Y^{**})V^{*-1}Z^*(Z^{*\text{T}}V^{*-1}Z^*)^{-1} .$$

Goldstein [166] showed that this can be written as

$$\text{cov}(\hat{\theta}) = 2(Z^{*\text{T}}V^{*-1}Z^*)^{-1} .$$

Using the current estimates of the fixed and random parameters, the IGLS procedure then iterates between Equations 5.5 and 5.6 [171]. As discussed previously, starting values for the fixed parameters are usually obtained from an OLS fit. On achieving convergence, under the assumption of multivariate Normality, the estimates are maximum likelihood.

5.3.5.2 Restrictive Iterative Generalised Least Squares

It is known that, in general, the IGLS procedure produces biased results [166]. This is especially problematic when the sample size is small. Alternatively, restricted iterative generalised least squares (RIGLS) can be used to obtain unbiased estimates. These are equivalent to restricted maximum likelihood estimates (REML) in the multivariate normal case [172]. Instead, $E(Y^*) = V$ is rewritten using the estimates of the fixed parameters, $\hat{\beta}$, to give

$$E(Y^*) = V - X\text{cov}(\hat{\beta})X^{\text{T}} = V - X(X^{\text{T}}V^{-1}X)^{-1}X^{\text{T}} .$$

From accounting for the sampling variation of $\hat{\beta}$, an unbiased estimate of V is obtained by adding the second term in the above expression at each iteration until convergence is obtained. The second term is the ‘hat’ matrix from Y^* and can be considered as a correction for bias [173].

5.3.5.3 Marginal and Penalised Quasi-likelihood

This section refers to Goldstein [166].

Consider a general 2-level model,

$$y_{ij} = X_{1ij}\beta_1 + Z_{1ij}^{(2)}u_{1j} + Z_{1ij}^{(1)}e_{1ij} + f(X_{2ij}\beta_2 + Z_{2ij}^{(2)}u_{2j} + Z_{2ij}^{(1)}e_{2ij}) + \dots ,$$

where f is a nonlinear function, X represents the fixed explanatory variables, $Z^{(1)}$, $Z^{(2)}$ are the random explanatory variables at levels 1 and 2 respectively, and the ‘ \dots ’ signifies that additional nonlinear functions, involving X or $Z^{(1)}$, $Z^{(2)}$ terms, may be included in the model. First, a suitable Taylor expansion is used to linearise the model. This produces a linear model where the explanatory variables in f are transformed using first and second derivatives of the nonlinear function.

Goldstein [166] shows that the nonlinear function, f , may be written as the sum of a fixed-part component and a random part. For the random part, the Taylor expansion up to a second-order approximation for the ij th unit is given by

$$f_{ij} = f_{ij}(H_{t+1}) + (Z_{2ij}^{(2)}u_{2j} + Z_{2ij}^{(1)}e_{2ij})f'_{ij}(H_t) + (Z_{2ij}^{(2)}u_{2j} + Z_{2ij}^{(1)}e_{2ij})^2 f''_{ij}(H_t)/2 .$$

Equation 5.7

The first term on the right-hand side of the above expression is the fixed part value of f at the current $((t+1)$ th) iteration of the IGLS (or RIGLS) algorithm. The other two terms are the first and second differentials of the nonlinear function, which are evaluated at the current values obtained from the previous iteration. From Equation 5.7 there is

$$E(Z_{2ij}^{(2)}u_{2j} + Z_{2ij}^{(1)}e_{2ij}) = 0, \quad E(Z_{2ij}^{(2)}u_{2j} + Z_{2ij}^{(1)}e_{2ij})^2 = \sigma_{zu}^2 + \sigma_{ze}^2 ,$$

$$\sigma_{zu}^2 = Z_{2ij}^{(2)}\Omega_u Z_{2ij}^{(2)T}, \quad \sigma_{ze}^2 = Z_{2ij}^{(1)}\Omega_e Z_{2ij}^{(1)T} .$$

The expansion for the fixed-part value in Equation 5.7 is written as

$$f_{ij}(H_{t+1}) = f_{ij}(H_t) + X_{ij}(\beta_{1,t+1} - \beta_{1,t}) f'_{ij}(H_t) ,$$

where $\beta_{1,t+1}$, $\beta_{1,t}$ are the current and previous iteration values of the fixed-part coefficients. H_t may be chosen to be the current value of the fixed-part predictor, $X_{2ij}\beta_2$. This is referred to as a ‘marginal’ quasi-likelihood (MQL) model. Alternatively, the current estimated residuals may be added when forming the Taylor expansion to give an improved approximation to the nonlinear component for each unit. This is referred to as a ‘penalised’ (or ‘predictive’) quasi-likelihood (PQL) model.

It is known that, in general, the MQL procedure tends to underestimate the values of the fixed and random parameters. This is especially a problem when the sample size is small [174, 175]; however, the PQL procedure has been shown to improve estimates [172]. Greater accuracy may also be obtained by using the second-order approximation rather than the first-order based upon the first term in the Taylor expansion. Therefore, improved estimates may be obtained using the 2nd-order PQL procedure. Intermediate choices include 1st-order PQL and 2nd-order MQL [150].

5.4 Multilevel Survival Modelling in MLwiN: Results

5.4.1 Introduction

This section will present results obtained by fitting multilevel survival models in MLwiN. As discussed previously in Section 3.5, the aim was to investigate the association between GHQ-12 score and first psychiatric hospital admission in Scotland, as measured in days from Scottish Health Survey interview. Some respondents may have had several psychiatric hospital admissions during follow-up; however, as interest was in modelling time until first psychiatric admission only, the multilevel structure for the models took the form of a single duration for each respondent, with respondents being nested within postcode sectors.

This chapter has discussed the use of both the proportional hazards model and the accelerated lifetime model for investigating the effect of covariates on survival time. Although the proportional hazards model, estimated using a Poisson model in MLwiN, is probably the most commonly used survival model, the use of the accelerated lifetime model may seem more intuitive when fitting multilevel survival models in MLwiN as it does not require creation of a person-period dataset. However, Yang & Goldstein [163] discussed that the quasi-likelihood under IGLS estimation procedure, used by MLwiN to estimate this model, is prone to breaking down when there are many censored observations. They suggested that this estimation procedure would not be recommended if there are more than 50% censored observations in the dataset. Recall that 99.1% of the observations in the SHeS dataset were censored. Thus, based on the advice from Yang & Goldstein, a multilevel accelerated lifetime model could not be fitted in MLwiN. As a result, only proportional hazards models will be used throughout this thesis when fitting survival models to the SHeS dataset in MLwiN.

To estimate the proportional hazards model, a two-level Poisson model with log link was fitted in MLwiN and a second-order polynomial was sufficient to smooth the blocking factors. The polynomial coefficients need not be interpreted since they are regarded as nuisance parameters. The response is the length of time in days from Scottish Health Survey interview, and observations were censored if the subject died or did not experience a psychiatric admission during follow-up. Note that the results presented in this section are for those respondents with no psychiatric hospital admissions prior to survey interview. For a further discussion of this see Sections 3.5 and 4.1.1.

For the continuous-time model, risk sets were defined for each failure time, which, in this example, was the time in days from survey interview at which a respondent was admitted to psychiatric facilities. This implied there were 136 risk sets for reasons discussed in Section 5.3.3.2. An offset was fitted in order to account for any tied observations. This was simply the logarithm of the number of failures in a particular time interval. In general, the offset was zero, since, as described above, there was only one interval at which there were tied observations.

Three separate models were fitted in order to investigate the association between GHQ-12 score and the hazard of psychiatric admission. Estimates of the fixed and random parameters with respective estimated standard errors are displayed in Table 5.3. Parameter estimates were obtained using IGLS and 1st-order penalised quasi-likelihood (PQL) approximation. IGLS was used as opposed to RIGLS since the sample size was large ($n=15305$), and 1st-order PQL was used rather than the preferred 2nd-order PQL method due to problems with convergence when trying to use the latter. For a discussion of estimation procedures see Section 5.3.5. The modelling strategy for the three models will be described below.

In Section 4.1.2, Table 4.5 showed that, subjectively, there appeared to be an increase in the percentage of respondents admitted to psychiatric facilities as GHQ-12 score increased. In order to investigate if this increase was significant, model B1, containing GHQ-12 score only and a random intercept for postcode sector, was fitted. Following this, it was then of interest to investigate if the association between increasing GHQ-12 score and an increased hazard of psychiatric admission remained after adjustment for a range of individual- and area-level demographic, socioeconomic and lifestyle risk factors.

As discussed in Section 3.2.1.2, GHQ-12 score is highly correlated with self-assessed general health in predicting mental health outcomes and therefore, in order to avoid potential over-controlling models were fitted both including and excluding self-assessed general health. Model B2 fitted all individual- and area-level risk factors apart from self-assessed general health and, finally, model B3 was fitted as in Model B2 but including self-assessed general health.

In order to investigate how much of the variation in the hazard of psychiatric admission between postcode sectors could be explained by individual characteristics, models B2 and B3 were at first fitted allowing only for the adjustment of individual-level risk factors. After removal of all non-significant individual-level risk factors, area-level risk factors (which included a measure of deprivation and a measure of urbanicity) were then added to the models. This allowed calculation of how much of the remaining variation in the hazard of psychiatric admission between postcode sectors was explained by these variables

when added to the models with all significant individual-level risk factors included.

Due to the large number of variables available in this dataset, Table 5.3 only displays results for significant individual- and area-level risk factors only. Table 2.1 provides a comprehensive list of all available risk factors.

5.4.2 Results from Multilevel Continuous-Time Hazard Model

Results from fitting the multilevel continuous-time hazard model via a Poisson model in MLwiN are given in Table 5.3. Results from checking the proportional hazards assumption are given in Appendix 2.

Results from model B1 concluded that there was a highly significant increasing trend in the hazard of psychiatric admission ($p < 0.001$) as GHQ-12 score increased. The between-postcode sector variation ($\sigma_u^2 = 0.255$) was large in comparison to the average hazard of psychiatric admission (for a person with a GHQ-12 score of 0) when accounting for GHQ-12 score ($\exp(\beta_0) = 0.00004$). The large between-postcode sector variation implied a greater similarity in the hazard of event for individuals within a postcode sector. Parameter estimates for the log hazard ratios in model B1 were similar to those for the log odds ratios in model A1 (Table 4.6). This is not unexpected, since it has been shown that the proportional hazards model and logistic regression model yield similar results when the outcome of interest is rare, in particular less than 5% [176]. Recall that 0.9% of individuals experienced the outcome of interest in this dataset.

Table 5.3 - Results from multilevel continuous-time hazard model

	Model B1 Estimate(s.e)	Model B2 Estimate(s.e)	Model B3 Estimate(s.e)
Fixed			
Intercept (β_0)	-10.173(0.165)	-10.684(0.317)	-10.866(0.333)
Log(t_{ij}) (α_1)	0.227(0.117)	0.227(0.117)	0.203(0.116)
Log(t_{ij}) ² (α_2)	0.089(0.061)	0.087(0.061)	0.076(0.061)
GHQ-12 Score			
0	0.000**	0.000**	0.000*
1-2 (β_1)	0.699(0.226)	0.571(0.228)	0.483(0.229)
3-4 (β_2)	0.964(0.278)	0.676(0.282)	0.535(0.286)
5-12 (β_3)	1.353(0.218)	0.944(0.227)	0.713(0.236)
Sex			
Male		0.000	0.000
Female (β_4)		-0.146(0.187)	-0.107(0.187)
Age			
16-24		0.000	0.000
25-34 (β_5)		-0.274(0.286)	-0.245(0.287)
35-44 (β_6)		0.009(0.277)	0.048(0.279)
45-54 (β_7)		-0.636(0.333)	-0.687(0.335)
55-64 (β_8)		-0.196(0.304)	-0.302(0.308)
65-74 (β_9)		0.161(0.384)	0.207(0.386)
Marital Status			
Married/cohabiting		0.000	0.000
Other (β_{10})		0.474(0.179)	0.390(0.181)
Receipts of Benefits			
No		0.000	0.000
Yes (β_{11})		0.801(0.200)	0.605(0.210)
Smoking Status			
Non-Smoker		0.000	0.000
Current Smoker (β_{12})		0.812(0.213)	0.722(0.215)
Ex-Smoker (β_{13})		0.035(0.300)	0.016(0.301)
Employment Status			
Full-Time		0.000	0.000
Unemployed (β_{14})		0.425(0.262)	0.541(0.267)
Part-Time (β_{15})		-0.365(0.253)	-0.317(0.254)
Self-Assessed Health			
Very Good			0.000
Good (β_{16})			0.505(0.225)
Fair (β_{17})			0.962(0.249)
Bad (β_{18})			0.191(0.553)
Very Bad (β_{19})			1.917(0.456)
Random			
Area Variation(σ_u^2)	0.255(0.263)	0.201(0.250)	0.246(0.247)

* $p_{\text{trend}} < 0.05$
 ** $p_{\text{trend}} < 0.001$

Following adjustment for all significant individual-level risk factors, apart from self-assessed general health, results from model B2 revealed that any GHQ-12 score of 1 or more remained significantly associated with an increased hazard of psychiatric admission ($p = 0.005$). The increasing trend continued to be highly significant ($p < 0.001$). In addition to having a GHQ-12 score of 1 or more, other significant individual-level risk factors associated with an increased hazard of psychiatric admission included not being married (i.e. single, separated, divorced or widowed), being in receipt of benefits and finally, being a current smoker. When added to the model including all significant individual-level risk factors, neither of the area-level risk factors was significantly associated with the outcome, and hence their addition did not explain any of the remaining variation between postcode sectors. Thus, the final version of model B2 contained (significant) individual-level risk factors only. The between-postcode sector variation in model B2 ($\sigma_u^2 = 0.201$) reduced from model B1 as a result of adjusting for further risk factors, with approximately 21% of the total unexplained variation between postcode sectors being explained as a result of going from model B1 to model B2.

Finally, following adjustment of all significant individual-level risk factors as well as self-assessed general health, results from model B3 indicated that, although the effect of GHQ-12 score on the hazard of psychiatric admission was attenuated when self-assessed general health was included, the increasing trend in GHQ-12 score remained significant ($p = 0.002$). Results from model B3 indicated that, in addition to a GHQ-12 score of 1 to 2 or 5 to 12, other significant individual-level risk factors associated with an increased hazard of admission included not being married (i.e. single, separated, divorced or widowed), being in receipt of benefits, being a current smoker, being unemployed, and having a self-assessed general health rating of other than 'very good'. Again, when the two area-level risk factors were added to the model containing all significant individual-level risk factors, neither was significantly associated with the outcome. Therefore, the final version of model B3 contained (significant) individual-level risk factors only. Just as in model A3 when logistic

regression was used, the between-postcode sector variation in model B3 ($\sigma_u^2 = 0.246$) increased from model B2 as a result of including self-assessed general health.

The possibility of over-controlling, if self-assessed general health was included in the model in addition to GHQ-12 score, was discussed earlier in this section and also more extensively in Section 3.2.1.2. Results from model B3, however, have shown that the increasing trend in the hazard of psychiatric admission still remained significant ($p = 0.002$) after inclusion of self-assessed general health. This suggested that both measures, in addition to each other, were still related to the outcome. Self-assessed general health was more strongly related to the outcome and therefore, if only one measure of potential psychiatric morbidity were available, this may be the better option. However, even after adjustment for self-assessed general health, GHQ-12 score still provided some information, implying that the two measures, used in combination with each other, were more powerful at prediction.

5.4.3 Summary

As discussed throughout this chapter, when fitting the continuous-time survival models to the SHeS data (with corresponding results displayed in Table 5.3), risk sets were defined for each failure time, which was the time in days from survey interview at which a respondent was admitted to psychiatric facilities. This discussion demonstrated that, in order to fit the Poisson models, the data had to be rearranged into a suitable form as shown in Table 5.2. Rearranging the data into this format meant that each respondent then had a line of data corresponding to each risk set they survived, and hence the size of the dataset expanded from 15305 respondents to just less than 1.9 million data points within respondents.

Defining risk sets for each failure time was not particularly problematic for the Scottish Health Survey dataset as its size ($n=15305$) was not exceptionally large. However, when considering much larger datasets, defining risk sets in this way may prove to be much more troublesome since, when rearranged, the expanded

person-period dataset will also be much larger. Larger datasets may lead to computational problems, either when trying to expand the data to create the person-period dataset in order to fit the Poisson models, or when trying to estimate the models in MLwiN. Therefore, alternative strategies for fitting survival models to larger datasets will be investigated. Chapter 7 reviews other methods which may be used as an alternative to continuous-time hazard models. Results obtained from the alternative methods will be compared with those in this chapter, which will be treated as the ‘gold standard’.

5.5 Use of Multilevel Survival Models in Previous Studies

This section will briefly review techniques adopted for fitting multilevel survival models to large datasets in other studies. Recall that the SHeS dataset consisted of 15305 individuals followed up for a maximum of 9 years. As this dataset is considered to be moderately-sized, with its purpose being to develop methods for fitting multilevel survival models to large datasets, other studies were only considered for review if datasets consisted of more than 15305 individuals and/or had a follow-up period greater than 9 years. This is because Section 5.4 demonstrated that multilevel continuous-time hazards models could still be fitted via Poisson models in MLwiN, suggesting that, even following data expansion, datasets of this size and follow-up period would not be problematic in MLwiN.

Around forty papers fitting multilevel survival models to real data were reviewed. However, from these, only ten papers met the criteria defined above and warranted inclusion in this section for discussion. The ten papers are summarised in Table 5.4 below. Note that the context of interest in the papers will not be covered here.

Table 5.4 - Summary of multilevel survival modelling literature with large datasets

	Author(s)	Size of Original Dataset	Length of Follow-up	Multilevel Statistical Model	Package
1	Yang et al.(2009) [177]	49154	30 years	Accel. Lifetime	MLwiN
2	Schootman et al.(2009) [178]	27936	9 years	PHM	MLwiN
3	Roberts(2008) [179]	34869	2 years	Discrete-Time	HLM
4	Chaix et al. (2007) [180]	341048	7 years	Cox PHM	R
5	Chaix et al. (2007) [181]	52084		Weibull	WinBUGS
6	Shih & Lu (2007) [182]	24798	1.5 years	Marginal Cox PH	
7	Dejardin et al. (2006) [183]	81268	17 years	Cox PHM	MLwiN
8	Krardal (2006) [184]	98992	10 years	Discrete-Time	MLwiN
9	Ma et al. (2003) [169]	574438	7.3 years	Cox PHM	C++
10	Merlo et al. (2001) [185]	38343	≈ 4 years	Logistic regress.	MLwiN

It can be observed from Table 5.4 that fitting multilevel survival models to large datasets (i.e. datasets with more than 15305 individuals) appears to be a recent development. All of the papers reviewed date from 2001 onwards, with only nine of the papers from 2003 onwards attempting to fit multilevel survival models to large datasets. Although Merlo et al. [185] were considering survival after initial hospitalisation for heart failure, they employed multilevel logistic regression models to carry out a survival analysis.

Of the remaining nine papers that did fit multilevel survival models, four used MLwiN, with a variety of different survival models being adopted. The most recent paper by Yang et al. [177] fitted multilevel accelerated lifetime models. As discussed in Section 5.3.4, no data expansion is required to fit the multilevel accelerated lifetime model in MLwiN, as is required when using a Poisson model to fit a Cox proportional hazards model. Therefore the multilevel accelerated lifetime model may be considered as a useful alternative to the semiparametric PHM in MLwiN when the dataset is large. However, as discussed in section 5.4, the quasi-Likelihood procedure used to estimate non-linear models in MLwiN fails (and is not recommended) if there is a high proportion of censored observations in the dataset. Yang et al. had a low proportion of censoring (around 10%) in their dataset, meaning multilevel accelerated lifetime models could be easily fitted in MLwiN. However, in the SHes dataset 99.1% of the data were censored,

and hence the use of multilevel accelerated lifetime models in MLwiN for this dataset would not be recommended.

Of the other three papers using MLwiN, other methods for fitting multilevel survival models included the use of discrete-time models and the proportional hazards model. Kravdal [184] used multilevel discrete-time hazard models to analyse a Norwegian dataset consisting of 98992 individuals. The follow-up time of 10 years was split into 6-month intervals, which the author deemed reasonable having compared results to when time was grouped into intervals of 3 months. A wider discrete-time interval led to fewer risk sets. Dejardin et al. [183] fitted a multilevel semiparametric proportional hazards model, which, in MLwiN, is fitted via a Poisson model, to analyse a French dataset consisting of 81268 individuals. Although time was considered to be continuous, the unit of time in this study (months), was larger than that considered in the SHeS dataset (days). A larger unit of time may lead to a greater number of tied failure times, and hence a smaller number of risk sets, thus resulting in a smaller dataset following expansion. Dejardin et al. also stratified analysis, breaking up the dataset into 12 separate cohorts which were analysed separately, with the largest cohort consisting of 28010 individuals before data expansion. A criticism of this paper is the estimation procedure adopted. First-order MQL was used to estimate the multilevel Poisson model; however, as discussed in Section 5.3.5.3, the MQL procedure may underestimate values of both the fixed and random effects. Greater accuracy is to be expected when the second-order approximation is used rather than the first-order, as adopted in this paper. Finally, Schootman et al. [178] used MLwiN to fit multilevel survival models to a dataset consisting of 27936 individuals; however, their analysis was stratified, hence breaking up the dataset into five cohorts which were analysed separately. The largest cohort then consisted of 7867 individuals. Models were estimated using PQL estimation.

Five of the ten papers reviewed here used packages other than MLwiN to fit multilevel survival models. Roberts [179] used the HLM6 program to fit multilevel discrete-time survival models to three separate cohorts, the largest containing 34869 individuals before data expansion. The size of this increased to 130961 following data expansion to obtain the person-period dataset. The follow-up time of 2 years was grouped into 8 intervals of unequal numbers of

days. In 2007, Chaix et al. [180, 181] wrote two separate papers using multilevel survival models to model large Swedish datasets. The first [180] concerned a dataset consisting of 341048 individuals, with a follow-up time of 7 years. The full dataset was split into two cohorts depending on the age of the individuals, thus leading to two cohorts comprising 192840 and 148208 individuals. The R software was used to fit multilevel Cox proportional hazards models which were estimated using a penalised likelihood method. The use of R for fitting multilevel survival models was reviewed by Kelly [167], who concluded that R was useful if only a single random effect was to be fitted. If more than one random effect was desired, R would not be suitable. In the paper by Chaix et al., individuals were nested within local areas; therefore, only one random effect was required, meaning the R software could be used. A possible disadvantage of R is that the random effect is limited to follow only a Gamma, Normal or t distribution. However, this is not as restrictive as MLwiN, where the random effect may only follow a (multivariate) Normal distribution. An advantage of the R software is that it is free to download from <http://www.r-project.org>. In their second paper of 2007 [181], Chaix et al. fitted a multilevel Weibull survival model to a dataset of 52084 individuals. Models were estimated in WinBUGS using Markov chain Monte Carlo (MCMC). WinBUGS was also reviewed in the paper by Kelly [167], who discussed how any number of random effects could be fitted, with a number of distributions being available for the random effects. WinBUGS is discussed further in Section 7.4. Ma et al. [169] fitted a Cox PHM to a dataset of 574438 individuals via a Poisson model using a program written in C++. Parameter estimates were obtained based on the orthodox best linear unbiased predictor approach. Finally, Shih & Lu [182] considered a dataset containing 24798 Nepali children. They fitted a two-level frailty model using a three-stage estimation approach. It is not clear which software was used to estimate the model.

5.6 Chapter Summary

This chapter has shown how commonly used single-level survival models, such as the proportional hazards model and the accelerated lifetime model, may be extended to include random effects to account for hierarchical clustering. The

use of several statistical packages for fitting multilevel survival models was considered in Section 5.3.2, with MLwiN being acknowledged as the most suitable package for fitting such models to a hierarchical structure. MLwiN is able to fit both the proportional hazards model and the accelerated lifetime model with the use of macros. As this thesis is concerned with fitting multilevel survival models to large datasets, it was of interest to see how MLwiN would perform when fitting multilevel survival models to such datasets. Section 5.4 displayed results obtained from fitting a multilevel proportional hazards model to data from the 1995 and 1998 Scottish Health Surveys (SHeS) in MLwiN. Interest was in measuring the association between GHQ-12 score and time until first psychiatric hospital admission as measured from survey interview, following adjustment for a range of demographic, socioeconomic and lifestyle risk factors. The event of interest was rare meaning that there was a high percentage of censored observations in the dataset (99.1%). In the presence of many censored observations, Section 5.4.1 discussed how the quasi-likelihood under IGLS estimation procedure tends to break down when fitting the multilevel accelerated lifetime model. As a result, this model was not appropriate for the SHeS data, and thus only the proportional hazards model was considered.

A multilevel continuous-time proportional hazards model was fitted to the SHeS data in MLwiN via a Poisson model with log link function. Detailed information of how the Poisson model was fitted in MLwiN was given in Section 5.3.3.1. In particular, this included a discussion about how each duration had to be expanded so that every individual had a series of records for each time point until either the event of interest or censoring occurred (known as the person-period dataset). This inevitably leads to an expansion in the size of the original dataset and, in the case of the SHeS dataset which consisted originally of 15305 individuals, creating the person-period dataset led to an expanded dataset consisting of approximately 1.9 million observations within individuals. MLwiN coped with fitting the multilevel Poisson model to these data; however, parameter estimates could only be obtained using the 1st-order PQL procedure instead of the preferred 2nd-order PQL procedure.

The SHeS dataset was viewed as a moderately sized dataset, and therefore did not prove to be too problematic. However, it can be envisaged that the data expansion resulting from creating the person-period dataset could be vast if the

size of the original dataset was already large (i.e. consisting of more individuals than the SHeS dataset), and therefore perhaps leading to problems with estimation. As health survey datasets are typically large, it is of interest to investigate more efficient ways to fit multilevel survival models to large datasets, and to ensure that these models are accessible to those working in public health. Using the SHeS dataset as a training dataset for developing and testing various methods, succeeding chapters will seek to establish the most efficient ways of fitting multilevel survival models to large datasets. Successful models will then be applied to a much larger dataset to confirm their effectiveness.

6 Discussion: Findings from the Scottish Health Survey

6.1 Introduction

The Scottish Health Survey (SHeS) dataset was linked with all psychiatric hospital admission and death records between 1981 and 2004 for the purpose of investigating the growing problem of mental disorder in Scotland. A review of the literature (Chapter 3) revealed that there was a lack of information available on risk factors for mental disorder in Scotland, and most of the literature reviewed came from studies conducted elsewhere.

In Scotland, most of the information on mental health comes from acute and psychiatric hospital discharge records. It therefore seemed appropriate to use psychiatric admission as a measure of poor mental health in Scotland. Using the linked SHeS dataset, it was possible to investigate risk factors for poor mental health in Scotland, where a psychiatric admission would be an indicator of poor mental health. The SHeS dataset contained information on a wide range of demographic, socioeconomic and lifestyle risk factors and the specific objective, using the SHeS data, was to investigate the association between the GHQ-12 (the questionnaire used to assess the psychosocial health of respondents in the SHeS) and psychiatric admission, while controlling for the numerous risk factors available in the SHeS.

Since the Scottish Health Survey dataset was hierarchical in nature, with respondents nested within postcode sectors, multilevel modelling techniques were employed to overcome the problems discussed in Section 1.2.

6.2 Summary of Findings

The outcome was time until psychiatric admission as measured in days from Scottish Health Survey interview. An unpublished Master of Public Health dissertation by Stewart [30] revealed that the likelihood of psychiatric admission

differed depending on whether the admission was a first admission or a readmission. Based on this finding, it was appropriate to stratify analyses according to whether or not respondents had any known history of psychiatric admission. No known history of psychiatric admission prior to survey interview implied that any psychiatric admission following survey interview was taken as a first ever admission. Similarly, if a respondent had a known history of psychiatric admission(s) prior to survey interview, then any admission following survey interview was taken as a readmission. For reasons given in Section 4.1.1, analyses focused only on risk factors for first psychiatric admission.

The first objective, as stated in Section 3.5, was to investigate the association between the GHQ-12 and first psychiatric hospital admission in Scotland. Table 4.5 in Section 4.1.2 suggested that, subjectively, there appeared to be an association between psychiatric admission and GHQ-12 score, with the indication of a possible increasing trend. This trend was investigated formally in Chapters 4 and 5 by fitting various multilevel logistic regression (Table 4.6) and multilevel survival models (Table 5.3). All results given in the tables listed indicated that there was a highly significant increasing trend in the hazard (odds for the logistic regression model in Table 4.6) of first psychiatric admission as GHQ-12 score increased. The between-postcode-sectors variation was always small (although it was large in comparison to the probability of psychiatric admission in the average area). This finding was consistent with the reviewed literature, where it was found by most that any variation between higher-levels, such as postcode sectors, was indeed very small (Section 3.4).

The second objective, as stated in Section 3.5, was to investigate whether any association between psychiatric admission and the GHQ-12 remained following adjustment for a range of individual- and area-level demographic, socioeconomic and lifestyle risk factors. There were a number of issues to consider before fitting the models. In public health and epidemiology, it is standard practice to control for sex and age when investigating the association between a set of risk factors and an outcome. In view of this, it was decided to include sex and age in every adjusted model, even if they were not significantly associated with the outcome in addition to the other predictors. The second issue concerned the over-controlling of variables in the models. Section 3.2.1.2 discussed how it had been shown that the GHQ correlated well with other self-

administered questionnaires. As information on respondents' self-assessed general health was available in the SHeS, there was the possibility of over-controlling if both GHQ-12 score and respondent's rating of their self-assessed general health were included in the model. In order to avoid this, models adjusting for other various risk factors were fitted both including and excluding self-assessed general health rating.

Fitting the various multilevel models (Tables 4.6 and 5.3) revealed that, when self-assessed general health was excluded, the increasing trend in the hazard (odds for the logistic regression model) of first psychiatric admission remained highly significant following adjustment for a range of, in the first instance, individual-level risk factors. Significant risk factors associated with an increased hazard of first admission (in addition to GHQ-12 score of one or more) included not being married (i.e. single, separated, divorced or widowed), being in receipt of benefits, and being a current smoker. Sex and age were not significantly associated with the outcome in addition to the other significant variables; however, they were included in the model for reasons discussed above. Employment status was bordering on significance; therefore, it was kept in the model. When the two area-level risk factors were added to the model including all significant individual-level risk factors, neither was associated with the outcome. The area-level risk factors comprised a measure of area deprivation (Carstairs score) and a measure of urbanicity. The multilevel logistic regression model indicated that this model explained 22% of the total unexplained variation between postcode sectors.

When the same models were refitted with self-assessed general health allowed as a potential risk factor, results were similar to those when self-assessed general health was excluded. The effect of GHQ-12 score on the hazard (odds for logistic regression model) was attenuated when self-assessed general health was included; however, the increasing trend remained significant. Significant individual-level risk factors also remained the same; however, this time, being unemployed, and having a self-assessed general health rating other than 'very good' (i.e. 'good', 'fair', 'bad' or 'very bad'), were also among the individual-level risk factors associated with an increased hazard (odds) of first psychiatric admission. Again, neither of the area-level risk factors was significantly

associated with the outcome when added to the model including all significant individual-level risk factors.

The results found here are not unexpected, and are fairly consistent with the literature. Section 3.3.1 highlighted discrepancies in the literature on the effects of demographic risk factors, such as sex and age, on mental disorder and psychiatric admission. Some authors reported significant associations between sex and mental disorder and age and mental disorder; other studies reported no significant associations. A number of studies conducted outside the UK [65, 72, 73] reported similar results to those found here, with no difference in admission to psychiatric facilities found between the sexes. A study conducted in the UK by Jarman et al. [66], which may be more comparable to the results found in this study of Scotland, also reported similar national psychiatric admission rates for men and women. However, a study conducted in England by Thompson et al. [75] did find differences in admission rates between the sexes, with higher rates being reported for males. The study by Thompson et al. was quite different from this study in that interest was in investigating patterns of psychiatric admission by age, gender, diagnosis and regional health authority, rather than investigating risk factors for psychiatric admission. Therefore they did not adjust for any socioeconomic or lifestyle predictors known to affect psychiatric admission. Thus, although the finding by Thompson et al. is not consistent with that found here in Scotland, the studies are not directly comparable. It may be somewhat surprising that sex was not found to be significant in this study as it has been suggested in the literature [68] that females suffer more from disorders that do not require hospitalisation (i.e. neurotic disorders). As a result, it may have been expected to find that males had a greater likelihood of psychiatric admission.

Marital status was found to be significantly associated with psychiatric admission in addition to a range of other risk factors. Indeed, it was shown that those in the 'not married' category, which included single, separated, divorced and widowed persons, had a higher likelihood of psychiatric admission than their married counterparts. This finding is consistent with the literature, with all of the reviewed literature reporting the lowest risk of mental disorder for married persons. It was also noted in the literature that married persons are more likely than single persons to be treated in the community [79]. It is therefore possible

that the significance of this risk factor only represents differing patterns of treatment (i.e. treatment in the community as opposed to inpatient admission) and not a greater likelihood of mental disorder.

In terms of socioeconomic risk factors for psychiatric admission, it is difficult to make direct comparisons between findings in this study and findings from other studies, as the range of socioeconomic factors varied between the studies reviewed. Apart from income, this study included all of the conventional measures of socioeconomic position (social class, education, material circumstances, employment status), whereas most of the reviewed literature included only one or two measures of socioeconomic status. An exception to this was the study by Lahelma et al. [58], which included a wide range of measures of socioeconomic position at childhood and adulthood. Indeed, Lahelma et al. commented that 'socioeconomic measures are not directly interchangeable and any single indicator is unlikely to provide a sufficient description of past and present socioeconomic circumstances'. Socioeconomic risk factors found to be associated with psychiatric admission in this study were receipt of benefits and employment status. Socioeconomic risk factors that were not significant in the model included social class of the chief income earner, years spent in education, top academic qualification and material circumstances. The latter corresponded to car and home ownership. It was not altogether surprising that a lot of these variables were not significant in the model in addition to each other, as high correlation between the variables is to be expected. For example, it would be expected that persons who spent the fewest years in education would have the lowest qualifications. This, in turn, may lead to poorer job opportunities, making car and home ownership difficult; or, indeed, the lowest qualified persons may be unemployed and thus receiving benefits. It is perhaps, therefore, somewhat surprising that both employment status and receipt of benefits were both significant in the model. The results indicated that unemployed persons and persons in receipt of benefits had an increased likelihood of psychiatric admission. It was not surprising that employment status was found to be significantly associated with the outcome, as there is a long history of interest in the association of this variable with mental disorder acknowledged in the literature [30, 87, 92, 96, 101]. If unemployment and receipt of benefits are taken to be representative of low socioeconomic position, then these findings

were in line with those of Kammerling & O'Connor [96] and Dekker et al. [97], who recognised a long-standing association between low socioeconomic position and admission to psychiatric hospital.

A number of 'lifestyle' variables such as average weekly alcohol consumption, smoking status and weekly participation in sports were also included as potential risk factors. Smoking status was the only lifestyle variable found to be significantly associated with first psychiatric admission in this study (Tables 4.6, 5.3). Again, it may not be surprising that not all of the lifestyle variables were significant in the model as there could be some correlation between them. For example, smoking status and alcohol consumption are usually correlated, with smokers tending to drink more and heavy drinkers tending to smoke more [186-188]. This unhealthy lifestyle may also imply that those persons would be less likely to participate in physical exercise. Findings from this study indicated that current smokers had an increased hazard (odds) of first psychiatric admission. No significant differences were found between non-smokers and ex-smokers. Findings from this study were consistent with those of Rasul et al. [108], Araya et al. [107] and Cuijpers et al. [105], who also reported a greater likelihood of mental disorder in current smokers. In addition, Araya et al. [107] reported no difference between non- and ex-smokers. However, these studies all referred to common mental disorders and therefore findings may not be directly comparable to those in this study if psychiatric admission is viewed more as a measure of major mental disorder. However, the study by Cuijpers et al. that found an association between common mental disorder and smoking found no association between smoking and incidence of major depression. On the other hand, Breslau et al. [106] did report an association between major mental disorder and smoking; however, they found an increased risk in both current and ex-smokers. A number of studies also suggested that the risk of mental disorder in current smokers increased even more as the number of cigarettes smoked increased [107, 108]; however, these data were not requested when applying to the Information and Services Division Scotland (ISD Scotland) for the Scottish Health Survey data to be used in this study (refer to Section 2.2 and Table 2.1).

As well as smoking status being an indicator of a poor or healthy lifestyle, it should be recognised that it may also be a measure of poor socioeconomic position. Many studies have reported that inequalities in smoking habits exist,

with low socioeconomic position being associated with a higher prevalence of smoking [189-192]. Smoking status has also been shown to be associated with a number of other measures of socioeconomic position. In particular, level of education [189-192] and occupational class [189, 190, 192] have been shown to be inversely associated with smoking status. These associations may also explain why not many of the socioeconomic risk factors in this study were significant in the model in addition to each other.

The final objective was to determine the ‘best’ threshold score for use of the GHQ-12 in Scotland. Section 3.2.1.1 noted that Goldberg suggested that a score of 1 or 2 was the optimal threshold score, as found by his original validity study in the UK in 1972 [45, 50]. However, many studies since this time suggested different threshold scores. As it is generally accepted that threshold scores vary between different settings, cultures and populations (reference list given in Section 3.2.1.1), it is not at all surprising that findings in the literature were inconsistent. In the published reports from the 1995 and 1998 Scottish Health Surveys [23, 25], a score of four or more was used to identify respondents with a high GHQ-12 score, and thus at risk of potential psychiatric disorder. However, using the 1995 and 1998 linked SHeS data, this study found that the hazard (odds) of first psychiatric admission was significantly increased in those scoring one or more in the GHQ-12 (Tables 4.6 and 5.3). This remained the case even after adjustment for a range of demographic, socioeconomic and lifestyle risk factors. Therefore, findings from this study suggest that a score of one or more is the ‘best’ threshold score for indicating high GHQ-12 score in the Scottish population. This fits in with Goldberg’s original validity study in the UK, as discussed in Section 3.2.1.1. However, if GHQ-12 is being used to predict the likelihood of psychiatric admission, then a threshold score of one or more would put a lot of people, perhaps falsely, at risk of psychiatric admission. Other studies have also reported that the GHQ-12 can produce a high rate of false positive results (Section 3.2.1.2), and therefore should be combined with other screening instruments. The combined use of the GHQ-12 and other screening instruments would also be recommended based on results from this study.

6.3 Limitations

6.3.1 Limitations of Data

Section 2.2 acknowledged that there could be weaknesses associated with using the linked SHeS-SMR04 dataset that could have implications for analyses. These weaknesses will now be considered. The first weakness is that of non-response to the survey interview. This is a potential source of bias since characteristics of responders may differ to those of non-responders. For the 1995 and 1998 SHeS, response rates to the individual survey interviews were 81% and 76% respectively. Generally it was found that women were more likely to respond than men, younger ages were the most likely to refuse and response rates decreased as level of urbanicity increased [23]. Weights were used in order to account for the differing rates of response between the sexes, age groups and regions. As with any survey, there were some respondents in the SHeS who refused to answer specific questions or have a biological measurement taken, thus leading to missing data. Furthermore, a small percentage of respondents (7-9%) refused permission to linkage. It may be that the decision to refuse, either to answering a question or to data linkage, is socially or geographically patterned which could bias results obtained from analysing these data. Using the 1998 SHeS dataset, Lawder et al. [27] investigated this notion by excluding all cases with missing values in any variables and reported that respondents for which complete survey data were available tended to be healthier (in terms of vegetable consumption, blood pressure, BMI measurements, general health and longstanding illness), less deprived, less likely to be on benefits, more likely to own their own home, better educated and of a higher social class. These findings suggest that refusal is socially patterned and that complete case analysis would lead to biased results since the sample would not be representative of the population of Scotland. It may be possible to overcome this by employing appropriate techniques for handling missing data, such as multiple imputation. This may lead to a more representative sample of the population of Scotland.

Another source of potential bias with using the linked SHeS-SMR04 dataset is emigration. As respondents to the SHeS are followed-up long after their survey interview, it may be possible that their SMR records are incomplete at the date

of linkage to the SHeS if they have emigrated subsequent to survey interview. Although emigration levels in Scotland generally tend to be low [22], there is a procedure in order to determine potential emigrants during the linkage process. This procedure involves linking the SHeS to the Community Health Index (CHI) in order to determine whether respondents are registered with a Scottish General Practice at the end of the SMR follow-up period [24]. Lawder et al. [27] reported that of the 15668 respondents to the 1995 and 1998 surveys who agreed to linkage, 15446 (98.6%) still linked to CHI in March 2005 (which is beyond the follow-up period for the Scottish dataset in this thesis). Although it is important to take emigration into consideration since characteristics of emigrants may be different to other individuals in the survey, Lawder et al. showed that including or excluding emigrants from modelling would only have a minimal impact on the results.

It is generally acknowledged that using cross-sectional data may be a limitation since it implies that no inferences about causal pathways can be made from the results [135, 137, 138, 140, 142]. Although the SHeS is cross-sectional, events are recorded following survey interview and therefore risk factors precede psychiatric admissions. However, as individuals who are mentally ill could be undiagnosed at the time of survey interview it is unclear as to whether risk factors precede psychiatric disorder. In particular, many studies have queried the direction of the relationships between marital status and mental disorder, and measures of socioeconomic circumstances and mental disorder. These queries will now be considered.

Marital status has been shown by many, as well as by this study, to be significantly associated with mental disorder, leading to the conclusion that persons in any category of marital status, other than married, were at higher risk of disorder (see Section 3.3.1 for references). However, as analyses were performed on cross-sectional data in most of these studies, authors were unable to comment on the direction of the association. Many authors have considered two hypotheses in an attempt to explain the association between mental disorders and marital status. They are most commonly known as the ‘selection hypothesis’ and the ‘protection hypothesis’. The selection hypothesis argues that constitutional traits of persons who develop mental disorders, even before its outbreak, may inhibit marriage [76, 81, 83, 193]. The protection hypothesis,

on the other hand, argues that marriage offers a degree of protection against conflict, even for those with constitutional traits, which in non-married persons may lead to an outbreak of mental disorder.

There are similar hypotheses attempting to explain the association between socioeconomic deprivation and mental disorder. These hypotheses are known as the social segregation hypothesis or ‘drift’ effect and the social causation hypothesis, or ‘breeder’ effect. The ‘drift’ effect argues that people already with a mental disorder are more inclined to move towards poorer areas, whereas the ‘breeder’ effect argues that factors, such as socioeconomic deprivation, encourage and exacerbate mental disorders [73, 83, 89, 194].

Similarly, there have also been suggestions of a ‘two-way’ relationship between smoking status and mental disorder; in particular, depression. Depression has been shown to be associated with initiation of smoking; conversely, however, it has also been shown that nicotine may increase the risk of mental disorder [195].

Another limitation of the linked SHeS dataset corresponds to the definition of ‘first psychiatric admission’. In this study, any admission recorded following survey interview was assumed to be a first admission if the respondent had no record of psychiatric admission prior to survey interview. However, psychiatric admission records were only available from 1981 onwards, and as a result information on any psychiatric admission(s) occurring prior to 1981 was unavailable. Consequently, when respondents were defined as having had no admission prior to survey interview, this definition only truly referred to having had no psychiatric admission since 1981. This issue is further affected by immigrants moving to Scotland from other countries. As information on any prior admissions outside of Scotland is unavailable, immigrants would be coded as having no prior psychiatric admission even though they may have been admitted to psychiatric facilities in their home countries. Similarly, individuals who migrate to other countries before the end of follow-up and subsequently experience a psychiatric admission in another country will have no outcome recorded (and will be censored when modelling the data using survival analysis).

6.3.2 Limitations of Variables and Analyses

A number of variables, suggested by the literature as being potentially important risk factors for mental disorder, were not available in this study. In particular, these included ethnicity and diagnostic group. Although ethnic group was recorded in the SHeS, the number of respondents classed in minority groups (i.e. non-white) was very small (<1%). It was therefore not possible to investigate the effect of ethnicity on psychiatric admission. As a result, this variable was discarded. Discarding this variable may have led to a loss of potentially important information since it has been shown by some that ethnic group may be associated with mental disorder [89, 96].

Diagnostic group has been shown by some to be associated with psychiatric admission; however, information on diagnostic group was not requested when applying for the SHeS dataset. Thompson et al. [75] found that depression and anxiety was the primary diagnosis given at admission, followed by schizophrenia and related psychoses. In addition, diagnosis has been shown to vary by gender. Both Timms [73] and Saarento et al. [74] discussed that, generally, dependencies and schizophrenia occurred more frequently in males, whereas neuroses and affective psychoses were more common in females. It may therefore have been of interest to investigate for a possible interaction between sex and diagnostic group, had information on diagnostic group been available.

As well as the suggestion of an interaction between diagnostic group and sex, there were a number of other potentially important interactions suggested by the literature. In particular, the most consistent findings included the following interactions. The first was between age and sex, where it was found by Thompson et al. [75] that the ages at which admission rates peaked differed for males and females; however, this was not supported by Kirshner & Johnston [72], who found no interacting effect of sex and age on admission. The second was between sex and marital status, where it has been suggested that the effect of marital status on admission differs by sex. It has been shown that males have higher rates of admission than females in every category of marital status except 'married', where it has been shown that males have lower rates of admission [82, 196]; however, Kirshner & Johnston [72] did not support this finding. There

was also the suggestion of a three-way interaction between sex, age and marital status [79, 80]. Due to time constraints, this study did not test for interactions between any combinations of variables since the purpose of the thesis was focussed more on the development of methods for fitting multilevel event history models, rather than providing a comprehensive investigation of psychiatric admissions.

Another interesting risk factor for admission which was not included in analyses, but possibly should have been, was survey year i.e. the year in which respondents took part in the SHeS, which would have been either 1995 or 1998. Although fitting survival models accounted for the differing lengths of follow-up time between the two surveys, inclusion of this variable may have demonstrated the changing patterns in psychiatric admission. If results had shown that respondents who took part in the 1998 survey had a smaller likelihood of admission than those in the 1995 survey, then this may have been a reflection of the shift from inpatient admission to treatment in the community.

In this study, the primary objective was to investigate the association between the GHQ-12 and first psychiatric hospital admission. However, there is a possible limitation with using this as the outcome measure. This concerns the changing patterns in psychiatric admissions with a shift from inpatient admissions to care in the community. In a study investigating geographical variations in the use of psychiatric inpatient services in New York, and how they have changed from 1990 to 2000, Almog et al. [197] noted that differences in rates of admission between certain population groups may have resulted from an inadequacy in access to community care. Thus, if people in more advantaged areas have better access to psychiatric care in the community and make use of this service instead of inpatient psychiatric care, then it may appear that admissions are higher in disadvantaged areas. Indeed, this study found that those of low socioeconomic position had a greater likelihood of psychiatric admission.

6.4 Recommendations for Future Work

A discussion of the limitations of this study in Section 6.3 suggested a number of recommendations for future work. The first recommendation concerns interactions between variables. Section 6.3.2 discussed a number of interactions between individual-level risk factors which were consistently found to be associated with mental disorder in the literature, but which were not investigated in this study. Therefore, this study could be developed further by including interactions between individual-level risk factors, random slopes to investigate how the association between each risk factor and first psychiatric admission varies across areas and cross-level interactions, i.e. interactions between individual- and area-level risk factors in the analyses.

Another recommendation concerns the outcome measure used. It should be decided before the study whether interest lies in investigating common mental disorder or serious mental disorder. Since the outcome measure here was psychiatric admission, this suggests that interest was in investigating more serious mental disorder, since, as has been discussed throughout the thesis, there is now the tendency to treat more common mental disorders in the community. This means that all findings from this study may only truly apply to serious mental disorders. However, if interest were in investigating risk factors for all mental disorders together, then GHQ-12 score might be a more appropriate outcome variable, since this study has shown that GHQ-12 score is associated with serious mental disorder, as well as common mental disorders, as was suggested by the literature.

Finally, if any further work was to be done with the same subset of Scottish Health Survey data as used in this study, it would perhaps be worthwhile reapplying to ISD Scotland for information on other potential risk factors of psychiatric admission. In particular, it may have been useful to have information on psychiatric diagnosis (and perhaps on the number of cigarettes smoked per day as discussed in Section 6.2).

6.5 Implications of the Findings

A literature review of risk factors for mental disorder and psychiatric hospital admission (Section 3.3) revealed that there was a paucity of information for the Scottish population and indeed almost all of the reviewed literature came from studies conducted outside Scotland. Although findings from studies conducted outside Scotland provide valuable information on risk factors for psychiatric admission, the generalisability of these findings to other populations, in this instance, the Scottish population, is always questionable since it is unlikely that risk factors affecting psychiatric admissions in one population will be identical to those in another. This may be a consequence of differences in management and diagnosis between populations. Therefore, one of the most important contributions that the findings from this study will make will be in providing a basis for which future studies of risk factors for psychiatric admissions in the Scottish population can refer to and build on. A proviso would be increased availability of information in Scotland. Increasing and expanding the amount of information on risk factors for psychiatric admission may have implications for both future research in studies conducted in Scotland and elsewhere, and future mental health policies and programmes in Scotland. For example, this study showed that low socioeconomic position was associated with first psychiatric admission. As a result, public health policies for mental health should, in particular, be targeting the most deprived individuals in Scotland. This may lead to a reduction in mental health inequalities between the poorer and more affluent socioeconomic groups.

Improving mental health may also lead to an improvement in other poor health behaviour, such as smoking. In this study smoking was shown to be associated with mental disorder, as measured by psychiatric admission. Smoking has been shown to be used as a 'coping mechanism' in order to manage depression and stress [191]; therefore, this would imply that an improvement in mental health may lead to a reduction in the need for coping mechanisms, such as smoking.

The primary finding of this study was that GHQ-12 score was associated with first psychiatric admission. With common mental disorders now tending to be treated in the community rather than in a hospital, psychiatric hospital admission is

perhaps more representative of more serious mental disorder. However, findings from the literature recommended that the GHQ only be used for detection of minor psychiatric disorder [49, 51, 58]; therefore, findings from this study are particularly interesting as they suggest that the GHQ is also associated with more serious mental disorder, as represented by a psychiatric admission. Hence, another implication of the findings is the use of the GHQ for detection of more serious mental disorders.

6.6 Conclusions

This study has shown that the GHQ-12 is significantly associated with first psychiatric hospital admission in Scotland, even after adjustment for a range of demographic, socioeconomic and lifestyle risk factors. Multilevel models allowed the variation in the hazard of first psychiatric admission to be partitioned into that attributable to differences between individuals and that attributable to differences between postcode sectors. The between-postcode sector variation was always found to be small, a finding that was consistent with the literature.

This study suggested that a score of 1 or 2 on the GHQ-12 was the optimal threshold score for defining psychiatric caseness in the Scottish population. This was consistent with Goldberg's original validity study carried out in the UK in 1972; however, it was perhaps not consistent with all of the other reviewed literature. This is not worrying given that variation in optimal threshold scores between different populations and cultures is to be expected, as was discussed in Section 3.2.1.1.

In conclusion, this study has provided a basis for which future studies of mental disorder in the Scottish population can refer to and build on, as well as highlighting groups most at risk of poor mental health, such as those of a low socioeconomic position. These groups need to be targeted in order to improve mental health in Scotland and reduce health inequalities between poorer and more affluent areas. The GHQ-12 may be used as a screening instrument to identify those at risk of potential psychiatric caseness for both common and more serious mental disorders.

7 Alternative Methods for Fitting Multilevel Survival Models to Large Datasets

7.1 Introduction

Chapter 5 discussed ways in which multilevel survival models can be fitted in MLwiN - a package specially designed for fitting multilevel models to hierarchical datasets. To fit a proportional hazards model, one of the most commonly used continuous-time survival models for modelling the effect of covariates on survival time, MLwiN adopts a Poisson modelling approach. As discussed in Section 5.3.3.2, a person-period dataset must be created in order to fit the Poisson model. This involves replicating each individual's record as many times as the observed number of time intervals, either until the event of interest or censoring occurs for that individual. Clearly, this leads to an expansion in the size of the original dataset which can become problematic for reasons discussed in Section 5.6. It is therefore of interest to investigate other methods which could be used as an alternative to fitting continuous-time multilevel proportional hazards models. Three possible alternatives will be considered in this chapter. These three methods will then be fitted to the SHeS dataset in order to test their effectiveness as alternatives to the continuous-time model. Results are given in Chapter 8.

7.2 Defining Different Risk Sets

7.2.1 Introduction

The first method to be considered, as an alternative to fitting continuous-time hazard models, involves defining different risk sets. When expanding the dataset in order to fit continuous-time hazard models, each individual event time was considered as a separate risk set. As a result, the size of the expanded dataset could become very large if there were a lot of events. Instead of considering each event as a separate risk set, one alternative is to consider all events

within, for example, a month or a year or any other length of time interval. This is achieved by dividing time into short intervals so that risk sets now correspond to each predetermined interval. Using this method involves fitting discrete-time models and it is expected that dividing time into short intervals and fitting discrete-time models will lead to a reduction in the size of the expanded dataset.

There are a number of other reasons why discrete-time models are favoured over continuous-time models. Firstly, accommodating tied observations (i.e. when two or more individuals experience the event of interest at the same time) is more straightforward using a discrete-time approach. In the SHeS data, tied observations were not a problem as there were so few events and the scale used to record time was so small (i.e. event times were recorded in days) making it unlikely that two or more individuals would have been admitted to psychiatric facilities at the same number of days from survey interview. However, if there are a lot of events in the dataset and the scale used to record time is longer, months, for example, then there is the potential for tied observations to occur. The use of continuous-time models in the presence of tied observations is inappropriate as inconsistent estimators can result [198]. Incorporation of time-varying covariates is also more straightforward using the discrete-time approach. Finally, following some restructuring of the data so that the response variable is binary (see Section 7.2.2), standard methods for fitting discrete response data, such as logistic regression, may be used to fit discrete-time models.

As mentioned above, the logit link function can be used to model the dependence of the hazard rate on time and explanatory variables; however, other link functions, such as the complementary log-log function, may also be used. If time is divided into meaningful discrete intervals, then the logit link is used; however, if an event occurs at an exact time, but the measurement of time is coarse (for example, if it is rounded to the nearest month), then this is referred to as grouped-time, and the complementary log-log link function should be used [199]. The complementary log-log link may also be preferred as the coefficient vector is invariant to the length of time intervals [156, 200]; however, the logit link may be favoured because of its computational convenience, and also because it is easy to interpret in terms of odds ratios [201]. Generally, however, the choice of link function does not matter as both

produce similar results, leading to the recommendation that the choice be based on ease of interpretation [202, 203].

7.2.2 The Multilevel Discrete-Time Model

7.2.2.1 Fitting Multilevel Discrete-Time Survival Models in MLwiN

Section 7.2.1 remarked that standard methods for fitting discrete response data may be used to fit discrete-time models. This means that any statistical package that can perform regression analysis of dichotomous response variables can be used to fit discrete-time hazard models. However, as the hierarchical structure of the Scottish Health Survey data must be incorporated into the model, a multilevel discrete-time model must be used. As discussed in section 5.3.2, MLwiN is a package specifically designed for fitting multilevel models; therefore, it is reasonable to use it to fit the (multilevel) discrete-time models.

Assuming that time is divided into p intervals (not necessarily of equal length), $\{I_t = [a_{t-1}, a_t]\}$ with $0 = a_0 < a_1 < \dots < a_p < \infty$, with discrete time $T=t$ where t in $\{1, \dots, p\}$ denotes an observed event in interval I_t . Then the discrete hazard function for individual i in postcode sector j is

$$g\{h(t|x_{ij(t)}; f(t), \beta, u_j)\} = \beta_0 + \sum_{p=1}^q \beta_p x_{pij(t)} + f(t) + u_j, \quad ,$$

where $x_{ij(t)}$ is a vector of (possibly time-varying) covariates, β is a vector of parameters to be estimated and represents the effect of the covariates on the baseline hazard (on the scale generated by $g(\cdot)$), u_j is the random-effect for postcode sector j , and is assumed to be Normally distributed with mean 0 and variance σ_u^2 , and, finally, $f(t)$ is a function of time used to model the baseline hazard function. Possible forms for $f(t)$ will be discussed in Section 7.2.2.3.

Because of its computational convenience and ease of interpretation, the logit link will be adopted as the link function for $g(\cdot)$ when fitting the multilevel discrete-time models in MLwiN. Therefore, the model can be written as

$$\log\left(\frac{h_{ij}(t)}{1-h_{ij}(t)}\right) = \log \text{it}(h_{ij}(t)) = \beta_0 + \sum_{p=1}^q \beta_p x_{pij(t)} + f(t) + u_j, \quad ,$$

Equation 7.1

where the logit-hazard, $\text{logit}(h_{ij(t)})$, refers to the log-odds of event occurrence in any time interval, given that the event has not already occurred prior to this time. This model is known as a proportional odds model. The proportional odds assumption will be discussed in Section 7.2.3. Petersen [157] noted that the coefficients estimated from a logit model may not be entirely comparable with those obtained from a continuous-time model; however, as discussed by Petersen, Willet & Singer [204] and Hank [205], if the conditional probability that an event occurs in time interval t (given that it has not occurred prior to this time) is small (Hank suggests no larger than 0.1), then the coefficients obtained from the discrete-time model will be similar to those obtained from the continuous-time model, and therefore the logit model can be viewed as providing a good approximation to the continuous-time proportional hazards model [205, 206].

In order to fit a discrete-time model, the data must first be expanded so that every individual's record is replicated as many times as the observed number of time intervals before experiencing the event of interest or being censored. As seen with the continuous-time data in Table 5.2, the original dataset can become very large after expansion; however, in the discrete-time case, time is restructured into intervals where each time interval represents a risk set, instead of treating each separate event time as a risk set as in the continuous-time case. This means that the expanded dataset in the discrete-time case will be smaller than in the continuous-time case since there will be fewer risk sets.

During the data expansion process, a set of dummy variables, $y_{ij(t)}$, are defined for individual i in group j so that

$$y_{ij(t)} = \begin{cases} 1 & \text{if event occurs at time } t \\ 0 & \text{otherwise} \end{cases}$$

Therefore, if an individual does not experience the event, they will have a sequence of zeros for every risk set, including a zero in the final risk set indicating they were ultimately censored. On the other hand, if an individual does experience the event, they will have a sequence of zeros for each risk set prior to experiencing the event, and then a value of one for the risk set during which the event occurred. Once an individual experiences the event, data collection terminates for this individual. Fitting a discrete-time hazard model is thus equivalent to fitting a binary response model on the expanded dataset. When the hazard is modelled using the logit link, the parameters represent the additive effects on the log odds of event.

Section 7.2.1 remarked that time-varying covariates could be easily incorporated into a discrete-time model. Time-varying covariates are covariates which change over time, such as age. The values of these covariates may vary between intervals, but should remain constant within each time interval. Time-varying covariates can be included in the model as interactions between fixed-time covariates and time [200]. A time-varying covariate implies that the proportional odds assumption is no longer valid. This will be discussed further in Section 7.2.3.

Because discrete-time models are fitted using standard models for binary response data, such as logistic regression, an approximate intraclass correlation (i.e. the proportion of the total variance that is accounted for by the higher-level units) may be calculated as follows:

$$ICC = \frac{\sigma_U^2}{(\sigma_U^2 + \sigma^2)} \quad .$$

When the logit link is used, the standard variance $\sigma^2 = \pi^2/3$ [203]. Alternatively, if the complementary log-log link is used, $\sigma^2 = \pi^2/6$ [203]. Further information on the intraclass correlation can be found in Section 4.2.

7.2.2.2 Determining the Length of Time Intervals

Section 7.2.2.1 discussed how the original dataset must be restructured so that each individual has a line of data corresponding to each risk set until failure or censoring occurs in order to fit the logistic model. As with continuous-time models (refer to Section 5.3.3.2 for information on data expansion in the continuous-time case), this restructuring inevitably leads to an expansion in the size of the original dataset. When time is grouped into discrete intervals so that there are fewer risk sets (with the number of risk sets being equal to the number of discrete-time intervals) than in the continuous-time case, the discrete-time person-period dataset still has the potential to be very large in size if the width of the intervals is short relative to the observation period [207, 208]. One way to reduce the size of this dataset is to increase the length of the intervals. This will lead to fewer intervals, hence fewer risk sets, and thus the size of the expanded person-period dataset will be reduced. Diamond et al. [209] found that little precision was lost by grouping durations into reasonably broad groups.

It should be noted also that each time interval need not be of equal length. If the data are restructured into time intervals corresponding to when event times occur, then each interval will vary in length. On the other hand, it may be appropriate to divide time into predetermined intervals, such as months, or calendar years, etc, depending on the nature of the study, thus leading to intervals of equal length.

7.2.2.3 Modelling the Baseline Hazard Function

In Equation 7.1 in Section 7.2.2.1, $f(t)$ was written to denote the baseline hazard function. Several forms can be considered for $f(t)$, as was also noted in Section

5.3.3.3. To recap, some of the possible forms, as discussed in Section 5.3.3.3, included fitting a polynomial function, blocking factors, or some parametric form could be assumed, such as the Weibull or Exponential distribution. When fitting the continuous-time models in Chapter 5, a polynomial function was used. It would not have been practical to use blocking factors in this case because of the large number of risk sets. Blocking factors are a set of dummy variables for the risk sets, written as

$$\alpha_1 Z_1 + \alpha_2 Z_2 + \dots + \alpha_l Z_l ,$$

where the α 's are parameters to be estimated and, for $g = 1, \dots, l$,

$$Z_g = \begin{cases} 1 & \text{for } t_g \\ 0 & \text{otherwise} \end{cases} .$$

As there are t_g or t_{g-1} dummy variables, using them in the continuous-time case would have meant that a large number of parameters would have to have been estimated. However, in the discrete-time case, where time has been grouped into a few intervals, it is recommended that the blocking factor approach be used [163]. In the logistic discrete-time model the α parameters thus represent the baseline hazard in each time interval as measured on a logistic scale.

7.2.3 Assumptions

As in the continuous-time case, fitting discrete-time models also requires a proportionality assumption. When a logit link is used as the link function, the proportionality assumption is termed the 'proportional odds' assumption. The proportional odds assumption is comparable to the proportional hazards assumption in a model for the log-hazard, and for it to be valid requires that the effect of a covariate is the same at all time points [199]. The proportional odds assumption is tested by including interaction terms between predictors and time in the model. The presence of a significant interaction implies non-proportionality, thus indicating that a covariate is time-varying.

As noted above, testing the proportional odds assumption is straightforward for single-level discrete-time models. However, as discussed in Reardon et al. [199] testing the proportionality assumptions becomes more complex in the multilevel case. Reardon et al. remarked that, as well as testing whether the effect of individual-level covariates on the hazard function is constant at all time points, testing whether the effect of higher-level covariates is constant at all time points must also be considered. They also discussed how multilevel models include an additional proportionality assumption, which they termed the ‘proportional error assumption’, the assumption that the higher-level error term for group j is constant at all time points. Full details of these assumptions and how they can be tested can be found in their paper.

7.2.4 Estimation

Maximum likelihood is the most widely used approach for estimating the parameters in the multilevel discrete-time model [201]. As the multilevel discrete-time model is non-linear, approximate estimation procedures are used. The two procedures available in MLwiN are marginal quasi-likelihood (MQL) and penalised quasi-likelihood (PQL). Refer to Section 5.3.5 for a full discussion of these procedures.

7.3 Grouping According to Covariates

7.3.1 Introduction

The second method to be considered as an alternative to fitting continuous-time proportional hazards models involves grouping individuals within postcode sectors according to values of their covariates and fitting continuous-time hazard models in MLwiN to the grouped dataset. This method entails grouping all individuals in the same postcode sector with the same values for covariates being fitted in a particular model and creating one line of data for these individuals as opposed to having a line of data for each individual. The concept

behind this method is that all individuals within the same postcode sector with the same values for covariates included in a particular model are at risk at the same time, and can therefore be represented by one line of data, so that the size of the expanded dataset can be reduced.

When individuals are aggregated according to their characteristics there is a slight change in the nesting structure. In the case of the SHeS dataset there are still two levels, with postcode sectors remaining at the higher-level (level 2). However, at level 1 there is now a pseudo-level of cells defined by each possible combination of the chosen characteristics. For example, in the case of model B1 (Table 5.3) where GHQ-12 is the only covariate in the model, each level 1 'cell' corresponds to one category of GHQ-12 score (score of 0, 1-2, 3-4 or 5-12). However, suppose the covariate 'sex' (where the choice is either 'male' or 'female') is added to this model. This means that there is now a cell corresponding to each GHQ-12 score/sex combination (i.e. 'score 0/female', 'score 1-2/female', . . . , 'score 5-12/male'). It is therefore envisaged that, as the number of covariates in a particular model increases, thus leading to an increase in the number of possible level-1 'cell' combinations, fewer individuals in each postcode sector will have similar cell characteristics. This implies that the percentage reduction in the size of the original continuous-time expanded dataset (Table 5.2) will not be as great as when only a small number of covariates (and hence fewer 'cell' combinations) are included in the model.

Another factor which can determine how effective this method is at reducing the size of the original continuous-time person-period dataset is the number of individuals within each higher-level unit. For a higher-level unit consisting of a large (small) number of individuals, there is a greater chance that there will be more (fewer) individuals within that higher-level unit sharing the same values of covariates and vice versa. This then leads to a bigger (smaller) reduction in the size of the expanded dataset as there would be more (fewer) individuals within a higher-level unit that could be grouped together by the values of their covariates.

As discussed above, this method involves fitting continuous-time hazard models to the grouped dataset, where individuals within the same postcode sector are grouped according to the values of their covariates. It is anticipated that

grouping individuals in this way will lead to a reduction in the size of the original continuous-time dataset (Table 5.2). However, it may be possible to reduce the size of the dataset even further by instead fitting discrete-time hazard models to the grouped dataset. As discussed in Section 7.2, fitting discrete-time hazard models involves dividing time into either intervals of equal length, such as calendar years, or intervals of varying length which are constructed corresponding to times when events occur. Adapting both continuous-time and discrete-time hazard models to be fitted to the grouped dataset, as well as a discussion of how to obtain the aggregated (grouped) dataset for both models, will be considered in Sections 7.3.2 and 7.3.3.

7.3.2 Continuous-Time Models

As discussed in Section 5.3, defining a response variable (indicating an observed failure or not) at each failure time for each member of the risk set leads to an expansion in the size of the original dataset, meaning that a continuous-time proportional hazards model can be fitted via a Poisson model in MLwiN. For individuals within the same postcode sector with the same values for the covariates in a particular model, this expanded dataset can be aggregated into one line of data, and the Poisson models can then be fitted to the aggregated dataset. Recall from Section 5.3 that the Poisson model included an offset, $\log(n_{gi})$, where n_{gi} is the total number of individuals that fail in a risk set across all postcode sectors, to account for any tied survival times. The offset is zero if there is only one failure during a particular risk set. When fitting the Poisson model to the aggregated dataset, a further term containing the number of individuals within a particular postcode sector with identical risk factors (i.e. the number of individuals in each cell) in a particular risk set is added. With the same notation as in Section 5.3, the model thus becomes

$$\log(\lambda_{gij}) = \log(x_{gij} + r_{gij}) + \log(n_{gij}) + \varphi(t_g) + \beta^T x_{ij} ,$$

Equation 7.2

where $\lambda_{gij} = (x_{gij} + r_{gij})\mu_{gij}$, x_{gij} is the number of individuals from the same postcode sector with identical risk factors who fail at time t_g , r_{gij} is the number of individuals from the same postcode sector with identical risk factors who survive at time t_g and μ_{gij} is the expected Poisson count in a given risk set. The algebraic derivation of this model is given in Section 7.3.2.1.

7.3.2.1 Algebraic Derivation

Recall from Section 5.3 that the log hazard of death for the i th individual at time t_g can be written as

$$y_{gij} = \log(d_{gij}) \approx \log(n_{gij}) + \log[(t_{g+\Delta} - t_g)h_0(t_g)] + \beta^T x_{ij} ,$$

where

$$y_{gij} \sim \text{Poisson}(\mu_{gij})$$

and therefore

$$\log(\mu_{gij}) = \text{offset} + \varphi(t_g) + \beta^T x_{ij} .$$

Refer to Section 5.3 for an explanation of notation.

Since $y_{gij} \sim \text{Poisson}(\mu_{gij})$, the likelihood function is given as

$$L(y_{gij} | \mu_{gij}) = \frac{(\mu_{gij})^{y_{gij}}}{y_{gij}!} \exp(-\mu_{gij}) .$$

If an individual fails at time t_g , then the response variable $y_{gij} = 1$ and the contribution to the likelihood is thus

$$L(y_{gij} | \mu_{gij}) = \mu_{gij} \exp(-\mu_{gij}) .$$

Otherwise, if the individual survives at time t_g , then the response variable $y_{gij} = 0$ and the contribution to the likelihood is then

$$L(y_{gij} | \mu_{gij}) = \exp(-\mu_{gij}) .$$

If x_{gij} individuals fail and r_{gij} individuals survive (say), from the same postcode sector and with identical risk factors, μ_{gij} will be the same for all such individuals and hence the contribution to the total likelihood is

$$\begin{aligned} L(y_{gij} | \mu_{gij}) &= (\mu_{gij})^{x_{gij}} \exp(-x_{gij} \mu_{gij}) \exp(-r_{gij} \mu_{gij}) \\ &= (\mu_{gij})^{x_{gij}} \exp[-(x_{gij} + r_{gij}) \mu_{gij}] \\ &= \frac{x_{gij}!}{(x_{gij} + r_{gij})^{x_{gij}}} \frac{[(x_{gij} + r_{gij}) \mu_{gij}]^{x_{gij}} \exp[-(x_{gij} + r_{gij}) \mu_{gij}]}{x_{gij}!} . \end{aligned}$$

Therefore

$$y_{gij} \sim \text{Poisson}(\lambda_{gij}) ,$$

where

$$\lambda_{gij} = (x_{gij} + r_{gij}) \mu_{gij} .$$

Hence

$$\begin{aligned} \log(\lambda_{gij}) &= \log[(x_{gij} + r_{gij}) \mu_{gij}] \\ &= \log(x_{gij} + r_{gij}) + \log(\mu_{gij}) \\ &= \log(x_{gij} + r_{gij}) + \log(n_{gij}) + \varphi(t_g) + \beta^T X_{ij} , \end{aligned}$$

since, as written above, and shown in Section 5.3, $\log(\mu_{gij}) = \log(n_{gij}) + \varphi(t_g) + X_{ij}\beta$. This is now Equation 7.2, the continuous-time hazard model to be fitted to the aggregated dataset, and the offset term is now $\log(x_{gij} + r_{gij}) + \log(n_{gij})$.

7.3.2.2 Obtaining the Aggregated Dataset

This section gives an overview of how the aggregated dataset is created from the original expanded dataset in MLwiN.

Before Equation 7.2 can be fitted, the original expanded dataset (Table 5.2) must be aggregated so that, for each risk set, there is just one line of data representing all individuals within the same postcode sector with the same values for the covariates in a particular model. The new response variable and the additional offset term, $\log(x_{gi} + r_{gi})$ must be also be created. Note that $x_{gi} + r_{gi}$ is the total number of individuals in a cell within postcode sector at the beginning of each risk set.

The first step in creating the aggregated dataset is to define the new level-1 units i.e. the cells within postcode sectors defined by each combination of the chosen covariates. For each risk set (where a risk set still corresponds to each specific event time), the number of individuals within a postcode sector with a particular covariate combination are counted and this creates the level-1 ‘cells’, giving the number at risk at the beginning of each risk set, i.e. $x_{gi} + r_{gi}$. If any cells are empty, i.e. there is no-one within a particular postcode sector with a particular covariate combination, then this cell may be omitted. Each cell within postcode sector is given a level-1 identifier. Next, the response variable (i.e. the number of individuals in each cell within postcode sector that are admitted during each risk set) is created. This is done by summing the response variable from the original expanded dataset, y_{gij} , for all individuals in each cell within postcode sector. This gives the number of psychiatric admissions in each risk set for each cell within postcode sector. n_{gi} , the number of people who fail in each risk set across all postcode sectors, is the same as in the original Poisson model fitted to the ungrouped continuous-time expanded dataset.

Following aggregation, the size of the original expanded dataset will be reduced; however, as discussed in Section 7.3.1, the percentage reduction will depend on the number of covariates being used for the grouping. Grouping on a larger number of covariates will lead to a smaller percentage reduction in the original expanded dataset.

7.3.2.3 Modelling the Baseline Hazard Function

Several forms are available for the baseline hazard function, $\varphi(t_g)$. Two common ways of estimating $\varphi(t_g)$, as discussed in Section 5.3.3.3, include fitting a polynomial function or using blocking factors. If there are a large number of time points, as may usually be the case when time is being treated as a continuous variable, fitting a polynomial function is the form recommended by Yang & Goldstein [163], as it avoids the need for estimating a large number of dummy variables, which would be the case if blocking factors were used. For a full discussion of modelling the baseline hazard function refer to Section 5.3.3.3.

7.3.3 Discrete-Time Models

Section 7.2 discussed how discrete-time hazard models, with time intervals of either equal or varying lengths, could be fitted as an alternative to continuous-time hazard models using a standard logistic model. The binary responses, indicating whether or not an individual failed in a given time period, followed a Bernoulli(π_{gij}) distribution. Fitting the logistic model in MLwiN still required use of an expanded dataset with each individual having a line of data corresponding to each risk set they survived. As time was grouped into intervals, instead of having a risk set for each distinct failure time as in the continuous-time case, the expanded dataset was much smaller than the original expanded continuous-time dataset; however, it was anticipated that this already smaller expanded dataset for fitting discrete-time hazard models could be reduced even further by aggregating it also so that there would be just one line of data representing all individuals within the same postcode sector with the same values of covariates in a particular model. This would mean, however, that the response, which would now be the proportion of individuals in a cell within postcode sector who failed in each risk set, would no longer follow a Bernoulli distribution as the denominator for the proportion, n_{gij} , would no longer be 1. Instead, n_{gij} would now correspond to the number of individuals in a risk set for each cell within postcode sector meaning that the responses would follow a Binomial(n_{gij} , π_{gij}) distribution. The algebraic derivation of the Binomial model follows in Section 7.3.3.1.

7.3.3.1 Algebraic Derivation

Recall from Section 7.2.2.1 that the logistic model for modelling π_{gij} , the probability of an individual failing in the current time period, given that they survived from the last period is written as

$$\log\left(\frac{\pi_{gij}}{1-\pi_{gij}}\right) = \log\text{it}(\pi_{gij}) = \varphi(t_g) + \beta^T x_{ij} \quad ,$$

where the actual binary response, y_{gij} , is 1 if the individual fails in the current time period, and 0 otherwise, and follows a Bernoulli(π_{gij}) distribution (i.e. a Binomial distribution with $n_{gij} = 1$).

Therefore, the likelihood function is given as

$$L(y_{gij} | \pi_{gij}) = \pi_{gij}^{y_{gij}} (1 - \pi_{gij})^{1-y_{gij}} \quad .$$

If an individual fails at time t_g , the contribution to the likelihood is thus

$$L(y_{gij} | \pi_{gij}) = \pi_{gij} \quad .$$

Otherwise, if the individual survives at time t_g , the contribution to the likelihood is then

$$L(y_{gij} | \pi_{gij}) = (1 - \pi_{gij}) \quad .$$

If x_{gij} individuals fail and r_{gij} individuals survive (say), from the same postcode sector and with identical risk factors, π_{gij} will be the same for all such individuals and hence the contribution to the total likelihood is

$$\begin{aligned} L(y_{gij} | \pi_{gij}) &= (\pi_{gij})^{x_{gij}} (1 - \pi_{gij})^{r_{gij}} \\ &= (\pi_{gij})^{x_{gij}} (1 - \pi_{gij})^{n_{gij} - x_{gij}} \quad , \end{aligned}$$

since $n_{gij} = x_{gij} + r_{gij}$.

Hence

$$y_{gij} \sim \text{Binomial}(n_{gij}, \pi_{gij}) .$$

7.3.3.2 Obtaining the Aggregated Dataset

As in Section 7.3.2.2, this section will just give a brief overview of how the aggregated dataset is created.

As with aggregating the data for the continuous-time model in Section 7.3.2.2, the discrete-time expanded dataset must again be rearranged so that, for each risk set, there is just one line of data representing all individuals within the same postcode sector with the same values for the covariates in a particular model. To fit the discrete-time model, the new binomial-distributed observed responses, y_{gij} , i.e. the proportion of individuals in each cell within postcode sector who fail within a given risk set and the denominator for the proportion, n_{gij} , corresponding to the number of individuals in a risk set for each cell within postcode sector, must be created.

Similarly to Section 7.3.2.2, the first step is to define the new level 1 cells within postcode sectors by counting, for each risk set (where this time a risk set corresponds to a specific time interval), the number of individuals within a postcode sector with a particular covariate combination. This also creates the denominator for the proportion, n_{gij} . Each cell within the postcode sector is given a level-1 identifier and again a cell may be omitted if there is no-one in that postcode sector with the specified covariate combination. Next, the response variable, y_{gij} , is created using the ungrouped discrete-time expanded dataset. Because, in the ungrouped discrete-time expanded dataset, each individual in a given postcode sector has a binary response taking the value '1' if the individual fails in a given time interval and the value '0' otherwise, the proportion of individuals who fail in a given time interval for each cell within postcode sector (i.e. the new response in the aggregated dataset) can be calculated by summing the values of the binary response variables at time t_g for all individuals within a particular cell within postcode sector, and dividing it by

the number of individuals in that cell within postcode sector (at time t_g). For example, suppose that at time t_g there are 4 individuals in a given cell within postcode sector with binary responses (0, 0, 1, 0), i.e. one person in this cell within postcode sector fails during this particular time interval (time t_g).

Therefore, the proportion of individuals in this cell within postcode sector who fail at this particular time is $(0 + 0 + 1 + 0)/4 = 1/4$, which is the new response, y_{gij} , in the aggregated discrete-time dataset.

7.3.3.3 Modelling the Baseline Hazard Function

In the case of discrete-time models, where time is grouped into intervals, blocking factors would be an appealing choice for modelling the baseline hazard function, $\varphi(t_g)$. There would be a blocking factor for each time interval. However, this choice may not be desirable if there are a lot of time intervals, and hence a continuous polynomial function may be used instead. A full discussion of this can be found in Section 5.3.3.3.

7.3.3.4 Determining the Length of Time Intervals

As discussed in Section 7.2.2.2, time intervals can either be constructed corresponding to when events occur, thus giving time intervals of varying length, or time can be divided into predetermined intervals, such as calendar years. Fewer time intervals will mean a greater percentage reduction in the size of the expanded dataset.

7.3.3.5 Estimation

Procedures for estimating non-linear models are discussed in Section 5.3.5.

7.4 Bayesian Survival Models

7.4.1 Introduction to Bayesian Multilevel Survival Models

To recap, interest in the Scottish Health Survey data involved investigating the association between psychosocial distress, as determined by the GHQ-12 and time until first psychiatric hospital admission in Scotland, which was measured in days from Scottish Health Survey interview. Previously, a multilevel Cox proportional hazards model was fitted via a Poisson model in MLwiN, and parameters were estimated using first-order penalised quasi-likelihood (PQL). This model may also be fitted using a Bayesian approach and estimated using Markov chain Monte Carlo (MCMC). However, as discussed in Section 5.3.3.2, the data must be rearranged so that each individual has a line of data corresponding to each risk set they survived before the Poisson models can be fitted. This can lead to a vast increase in the size of this new expanded dataset, especially if the size of the original dataset before expansion is already large, meaning that models will take a long time to run when MCMC methods of estimation are used, and certainly longer than when PQL methods are used. However, there are advantages in using a Bayesian approach over a frequentist approach, especially for random-effects models due to the connection between them and Bayesian hierarchical models, and of using MCMC methods of estimation over maximum likelihood methods. These advantages will be briefly considered here.

One of the main advantages of using a Bayesian approach over a frequentist approach is that, in addition to the sampling distribution, $P(x|\theta)$, it allows any prior knowledge about the value of θ (obtained, for example, through previous experiments or research), where θ represents some quantity of interest, to be incorporated into analysis as a probability density function, $P(\theta)$.

Given these two distributions, the joint distribution of (θ, x) can be constructed as follows:

$$P(\theta, x) = P(x|\theta)P(\theta).$$

The likelihood function, $P(x|\theta)$, provides the chances of each value of θ having led to the observed value of x and the prior density contains the probability

distribution of θ before observation of the data, x [210]. However, observing the data changes the information about a parameter, and therefore inference should be based on the probability distribution of θ after observing the data. This distribution is known as the posterior distribution, and can be obtained via Bayes' Theorem:

$$P(\theta|x) = \frac{P(x|\theta)P(\theta)}{P(x)} \\ \propto P(x|\theta)P(\theta) .$$

where

$$P(x) = \int P(x|\theta)P(\theta) d\theta .$$

Equation 7.3

A 'drawback' of the Bayesian approach, especially for non-linear models such as the proportional hazards model, is that the likelihood function does not have an analytical form, and there can be difficulty integrating the required integrals. Previously, numerical integration or analytical approximation techniques would be required for parameter estimation in such models; however, with the recent advances in computing technology, techniques such as Markov Chain Monte Carlo (MCMC) may be used as an alternative to traditional approaches. MCMC will be discussed further in section 7.4.5.1.

Bayesian inference using MCMC methods has several advantages over frequentist approaches. Firstly, unlike the frequentist approach, which relies heavily on asymptotic approximation and can raise the issue of whether the sample size is large enough for these approximations to be valid, Bayesian inference allows exact inference for any sample size [211]. Secondly, Bayesian inference using MCMC allows more complex models to be fitted straightforwardly. For a thorough comparison of Bayesian and likelihood-based methods for fitting multilevel models, refer to Browne & Draper [212].

Although there is a large amount of literature available on the proportional hazards model, very little of this involves Bayesian inference [213]. This has mainly been because of computational limitations; however, as discussed above, MCMC methods, which are now much more accessible using packages such as

WinBUGS, make estimation of previously intractable models more straightforward.

It was discussed above that, although the Poisson model fitted in MLwiN could be fitted using a Bayesian approach and MCMC methods of estimation; MCMC methods would prove to be very slow because of the large person-period dataset required to fit the Poisson model. However, as an alternative, WinBUGS allows frailty models to be fitted to multilevel survival data. As the frailty modelling approach does not require any data expansion, estimation of these models may be faster. Frailty models are discussed in Section 7.4.2. For a brief review of previous research on frailty modelling from both a frequentist and a Bayesian viewpoint, refer to Sargent [214].

7.4.2 Frailty Models

7.4.2.1 Introduction to Frailty Models

The term ‘frailty’ was originally suggested by Vaupel et al. [215] in the case of univariate survival data and by Clayton [216] for bivariate data. For univariate data, the frailty is a random effect used to represent unobserved population heterogeneity among individuals, i.e. the influence of unobserved or unmeasurable risk factors, in univariate survival analysis [217-219]. Clayton [216], on the other hand, studied pairs of related individuals (e.g. fathers and sons), and included a parameter to measure the association arising when two members of a pair share some common influence. More recently, frailty models have also become popular for modelling multivariate survival data. Multivariate survival data may also be referred to as ‘correlated survival data’ or ‘clustered data’ [161]. There are two ways in which survival times may be correlated/clustered (note that these terms will be used interchangeably throughout the thesis). Firstly, observations may be clustered in a way that introduces an association between the individual survival times within a cluster; for example, individuals within a postcode sector, as in the Scottish Health Survey, may have some unmeasured environmental factors in common [220, 221]. Secondly, if several events are measured on the same person (recurrent

event data) then correlation between events within an individual would be expected [220]. In the case of multivariate survival data, the frailty represents an unobserved random effect shared by individuals within a cluster [160]. Frailty models are mixed models or random effects models for survival data where the frailty variable, assumed to act multiplicatively on the hazard function, models the dependence between survival times [222-224]. The frailty term allows individuals in the same cluster to share a common baseline hazard function, but allows this hazard function to differ between clusters [214]. Because the frailties act multiplicatively on the baseline hazard, they are interpreted as relative risks. The most common type of frailty model for modelling correlated survival data is the so-called ‘shared frailty model’. The shared frailty model will be discussed in Section 7.4.3.

7.4.3 The Shared Frailty Model

The shared frailty model is a conditional independence model in the sense that event times of individuals within a cluster are independent, conditional on the frailty terms [161, 220]. The model assumes two sources of variation - the group variation, which is described by the frailty, and individual random variation, which is described by the hazard function [161].

The hazard at time t , conditional on the frailty, w , is assumed to be the product of the frailty and a baseline hazard, $h_0(t)$, such that

$$h(t | w) = wh_0(t) \quad .$$

The shared frailty model is, in fact, an extension of the proportional hazards model therefore allowing covariates to be incorporated into the model. Thus, the hazard function at time t_{ij} , where T_{ij} is the survival (failure) time of the i th subject ($i = 1, \dots, n$) in the j th cluster ($j = 1, \dots, m$), given the unobserved frailty parameter, w_j , and fixed observed covariate vector, x_{ij} (which may be time dependent), is

$$h(t_{ij} | x_{ij}, w_j) = h_0(t_{ij})\exp(\beta^T x_{ij}) w_j \quad .$$

The frailty random variables, w_j , are assumed to be independent and identically distributed for each cluster, and typically follow some parametric distribution with unit mean and unknown variance, σ_w^2 . Any positive distribution can be chosen to model frailty [225]. However, there are some common choices in the literature which will be considered in Section 7.4.3.1. The mean is constrained to be one in order to make the baseline hazard function identifiable. The baseline hazard function can then be interpreted as the hazard rate of an ‘average individual’ [226]. Thus, individuals with frailty greater than one have an increased hazard of failure and vice versa. The unknown variance parameter, σ_w^2 , measures the between-cluster variation. A variance of zero implies that individuals within the same cluster are independent, whereas a larger variance means greater variability in frailty between clusters i.e. a greater correlation of survival times of individuals within the same cluster [224].

Because the shared frailty model is an extension of the proportional hazards model, there is flexibility in modelling the baseline hazard function. Shared frailty models may be parametric, where both the frailty and baseline hazard function follow some (positive) parametric distribution; or semi-parametric, where a parametric distribution is specified for the frailty only and the baseline hazard function is left completely unspecified. Various approaches to modelling the baseline hazard function, as well as advantages and disadvantages with following a particular approach, are discussed in section 7.4.3.2.

7.4.3.1 Choice of Frailty Distribution

This section provides a brief review of some possible choices for the frailty distribution. A more comprehensive review of possible parametric choices can be found in Hougaard [161] and Ibrahim et al. [221].

The conventional distribution for modelling the frailty term is the gamma distribution [161, 218, 224, 225, 227-229]. The most common reason for using the gamma distribution, as described in the literature, is its mathematical convenience. This is due to the simplicity of the derivative of the Laplace transform, meaning that traditional maximum likelihood procedures can be used

for parameter estimation [161, 225]. Its flexible shape is another reason given for selection of the gamma distribution as the frailty distribution [228, 229]. Although it may be the most commonly used frailty distribution for the mathematical reasons here described, Hougaard [218] emphasised that there are no biological reasons for choosing the gamma distribution. There are, however, some disadvantages of the gamma distribution. Clayton [230] described that the marginal relationship between the hazard and covariates does not follow the proportional hazards model, and that there is a convergence of hazards. Instead, the positive stable distribution has been recommended as an alternative frailty distribution as it avoids this problem [161, 230]; however, as noted by Hougaard [161], the derivatives of the Laplace transform are more complicated than with the gamma distribution, making parameter estimation more complicated. However, Bayesian methods using MCMC estimation can offer an alternative to traditional frequentist methods of estimation [221]. Bayesian methods of estimation will be discussed in Section 7.4.5.

The log-normal distribution has also been used and recommended by some authors as the frailty distribution [161, 214, 220, 222, 225, 226, 228, 231-233]. If u_j ($j = 1, \dots, m$) follows a normal distribution, where the frailty variable is defined as $w_j = \exp(u_j)$, then w_j follows a log-normal distribution. However, unlike the mathematically attractive gamma distribution, where an explicit representation of the likelihood function is always available [225], a closed-form expression for the observed data likelihood is not allowed by the log-normal distribution [226]. This means that more sophisticated methods of estimation must be used. If a frequentist estimation approach is being used then the Laplace transform and its derivatives can be approximated ([161, 233] for a summary of frequentist methods); however, Bayesian MCMC methods may be applied (see Section 7.4.5).

Although this section has so far discussed how it is customary for the frailty random effect to follow some parametric distribution, a small number of authors have, in fact, considered a nonparametric frailty distribution [234-236]. It has been argued that misspecification of the random effects (where random effects are defined to be the logarithms of the frailties) could lead to poor estimates of the parameter of interest. When the frailty distribution or random effects distribution is modelled nonparametrically, the distribution is left completely

unspecified, with the only assumption being that it is finite [236]. Naskar [236] adopted a semiparametric model in that the hazard function was modelled parametrically with the distribution of the frailty being modelled nonparametrically using a Dirichlet process. Dos Santos et al. [234] also adopted a semiparametric approach with a parametric hazard and nonparametric frailty; however, they did advise that a fully nonparametric approach (i.e. nonparametric hazard and frailty) would be preferred, but that this approach is limited by computational limitations and identifiability problems. Since then, however, Walker & Mallick [235] did manage to adopt a fully nonparametric approach by leaving the baseline hazard function completely unspecified, and using Pólya trees as a Bayesian nonparametric prior for the random effects distribution. Bayesian MCMC methods were used to overcome computational limitations, and they argued that the identifiability problem was solved using Pólya trees. Pólya tree distributions are generalisations of Dirichlet processes [237]. Detailed information on Pólya trees can be found in Lavine [237, 238] and Mauldin et al. [239].

It has been argued that the choice of frailty distribution may be relatively unimportant [217, 223, 228, 231, 233, 240]. In particular, Sastry [228] reported that results were ‘unlikely to be sensitive to the choice of frailty distributions when the proportion of the population surviving the period of analysis is high, unless the variance of the frailty distribution is large’. However, Hougaard [161] argued that the choice of frailty distribution depends on the problem, and that model properties of each distribution should be considered as relevant. With this in mind, Hougaard [161, 218] compared the properties and the fit of some commonly used frailty distributions.

7.4.3.2 Modelling the Baseline Hazard Function

Section 5.2 described how the baseline hazard function of the proportional hazards model can be modelled either parametrically or non-parametrically. As discussed throughout this section, the shared frailty model is an extension of the proportional hazards model in that, conditional on the frailty, event times follow the usual proportional hazards model. This implies that the baseline hazard

function may be modelled nonparametrically or parametrically. In terms of modelling the baseline hazard function parametrically, Hougaard [161] acknowledged the Weibull model as the most natural choice of parametric distribution as it allows for the proportional hazards model and the accelerated lifetime model. The Weibull model will be discussed further in Section 7.4.4 as the modelling strategy used by WinBUGS to fit the shared frailty model involves fitting an additive frailty model with Weibull hazard.

Although the baseline hazard function may be modelled parametrically, some have argued that the parameters of the frailty distribution may be sensitive to the choice of distribution for the hazard, and that the choice of distribution for the hazard may, in fact, be more important than the choice of frailty distribution [223, 234]. On account of this argument, it may be better to model the baseline hazard function nonparametrically and leave it completely unspecified. This would mean adopting a semiparametric approach if the frailty follows some parametric distribution, as is usually the case, or a fully nonparametric approach if the frailty is also being modelled nonparametrically (see Section 7.4.3.1). A nonparametric distribution for the hazard function has been used by Klein [241] in a frequentist framework and by Clayton [230] in a Bayesian framework. Sinha & Dey [242] also considered different ways of Bayesian modelling for nonparametric parts of the frailty model, such as the baseline hazard function.

7.4.4 Fitting Frailty Models in WinBUGS

Section 7.4.1 remarked that multilevel survival models using a Bayesian framework could be fitted in packages such as WinBUGS. WinBUGS, an acronym for ‘Bayesian Analysis Using Gibbs Sampling’ aims to make practical MCMC methods available to applied statisticians and is an ideal package to use as it can be downloaded free of charge from <http://www.mrc-bsu.cam.ac.uk/bugs/winbugs/contents.shtml>, making its use readily available. WinBUGS 1.4 is the current (Windows) version of the package it and can be readily applied to implement the shared frailty model. To fit the frailty model, WinBUGS assumes a parametric Weibull distribution for the survivor function.

Suppose that (r, γ) are the parameters of the Weibull distribution. Then the hazard function is given by

$$h(t_{ij} | x_{ij}, w_j) = \gamma r w_j t_{ij}^{r-1} \exp(\beta^T x_{ij}).$$

This model is a multiplicative frailty model; however, the modelling strategy adopted in WinBUGS is based on an additive frailty model. The additive frailty model is achieved by writing

$$h(t_{ij} | x_{ij}, u_j) = \mu_{ij} r t_{ij}^{r-1},$$

Equation 7.4

where

$$\log(\mu_{ij}) = \alpha + \beta^T x_{ij} + u_j.$$

Exponentiating this leads to the parameterisation

$$t_{ij} \sim \text{Weibull}(r, \mu_{ij}),$$

for $i = 1, \dots, n$ and $j = 1, \dots, m$. The shape and scale parameters of the Weibull distribution are denoted by r and μ_{ij} respectively. The shape parameter, r , allows the hazard function to increase or decrease with increasing time, and is interpreted as follows: for $r < 1$ the hazard rate strictly decreases in a nonlinear pattern as time increases; for $r = 1$ the hazard rate is constant (and the Weibull and exponential survival probabilities are the same); and, for $r > 1$, the hazard rate is strictly increasing in a nonlinear pattern as time increases [243]. The u_j 's are the additive random effects in the exponent of the hazard model and are assumed to follow a normal $(0, \tau)$ distribution. In fact, the additive frailty model is actually a multiplicative frailty model with a log-normal frailty distribution; therefore, the additive and multiplicative frailty models should yield similar inferences [221, 244].

7.4.4.1 Fitting the Weibull Model to the Scottish Health Survey Data

The association between the GHQ-12 and the hazard of first psychiatric hospital admission in Scotland can be investigated using frailty models, which were fitted in WinBUGS via a Weibull model with a log-normal frailty distribution.

Recall that the SHeS dataset consisted of 15305 individuals within 624 postcode sectors; therefore, the model is given by

$$t_{ij} \sim \text{Weibull}(r, \mu_{ij}),$$

for $i = 1, \dots, 15305$ and $j = 1, \dots, 624$. Thus, if taking a GHQ-12 score of 0 as the baseline, the model is written in WinBUGS as follows:

```

Model (1)
{ (2)
# Level 1 (3)
for (i in 1:15305) { (4)
time[i] ~ dweib(r,mu[i]) I(censor[i],) (5)
log(mu[i]) <- alpha (6)
+ beta[1]*score_1_2[i] (7)
+ beta[2]*score_3_4[i] (8)
+ beta[3]*score_5_12[i] (9)
+ u2[area[i]] (10)
} (11)
# Random effects: (12)
for (j in 1:n2){ (13)
u2[j] ~ dnorm(0.0, tau.u2) (14)
} (15)
}

```

The u_i 's are the additive random effects for postcode sectors in the exponent of the hazard model and are assumed to follow a normal $(0, \sigma_u^2)$ distribution. In WinBUGS, the variance of the normal distribution is written in terms of the precision, τ , where $\tau = 1/\sigma_u^2$.

In line 5 of the above WinBUGS code, it can be seen that the distribution for time is expressed as $\text{time}[i] \sim \text{dweib}(r, \mu[i]) I(\text{censor}[i],)$. This indicates that, for the censored observations, the survival distribution is a truncated Weibull distribution, with lower bound corresponding to the censoring time [245].

The regression coefficients, shape parameter and the random effects variance are given non-informative priors. Choice of priors will be discussed in Section 7.4.4.2 below. Bayesian estimation of the parameters, as performed in WinBUGS, is discussed in Section 7.4.5.

Following estimation of $\log(\mu_{ij})$, the hazard function of the additive hazard Weibull model is calculated as shown in Equation 7.4. It may also be of interest to calculate other properties, such as the mean survival time.

If the survivor function is distributed as Weibull, then the mean survival time is given as

$$E(t) = \mu^{-1/r} \Gamma(1 + 1/r),$$

where Γ represents the gamma function.

The survivor function is given as

$$S(t) = P(T \geq t) = \exp(-\mu t^r).$$

7.4.4.2 Priors

Unlike the frequentist approach, the Bayesian approach allows any prior knowledge about the value of θ , where θ represents some quantity of interest, to be incorporated into analysis as a probability density function. As seen in Equation 7.3 in Section 7.4.1, Bayes theorem can be written as

$$P(\theta | x) \propto P(x | \theta)P(\theta),$$

where $P(\theta | x)$ is the posterior distribution, $P(x | \theta)$ is the likelihood function, and $P(\theta)$ is the prior distribution. Prior distributions must be specified for all unknown parameters in the analysis. The frailty model is a hierarchical model, and therefore involves several levels of conditional prior distributions, where the dependence between the θ 's is accounted for by modelling them as conditionally independent given some hyperparameter.

There are a number of cases in which it may not be desirable to incorporate prior information into the analysis. Firstly, prior information on θ may not be available; or it may be preferable to let the data dominate; or, finally, MCMC methods may just be being used for computational convenience and hence the inclusion of prior information may not be desired [246]. In these cases, ‘vague’ or ‘reference’ priors may be used. Vague priors are also commonly referred to as ‘diffuse’ or ‘non-informative’.

In this thesis, MCMC methods have been adopted for computational convenience since fitting multilevel survival models via Bayesian frailty models in WinBUGS does not require the data expansion required to fit multilevel survival models via a Poisson model in MLwiN. With this in mind, vague priors were adopted for all parameters and hyperparameters. In the Weibull model (code given above), priors must be specified for the regression coefficients, β_k ($k = 1, 2, 3$) and the random effects, u_j ($j = 1, \dots, 624$), as well as a hyperprior for the random effects variance, σ_u^2 , and a prior for the shape parameter, r , of the Weibull distribution.

It is assumed that the GHQ-12 scores in the SHeS are representative of GHQ-12 scores in the Scottish population, and therefore beta regression coefficients were assigned independent vague Normal priors with zero mean and precision 0.0001,

$$\beta_k \sim \text{Normal}(0, 0.0001), (k = 1, 2, 3).$$

Recall that the betas represent logarithms of relative risks.

For the shape parameter of the Weibull distribution, Spiegelhalter et al. [245] used a $\text{Gamma}(1, 0.0001)$ prior which is slowly decreasing on the positive real line; however, assigning a Gamma prior to the shape parameter when fitting the model to the SHeS dataset tended to cause ‘trap’ messages in WinBUGS. Trap messages correspond to an error which has not been picked up by WinBUGS [245], and generally these messages are difficult to decode, especially for novice users. However, suggestions on how to interpret some common trap messages are given in the WinBUGS manual [245].

Instead, a vague log-Normal prior with mean one was assigned such that,

$$\log(r) \sim \text{Normal}(0, 0.1) .$$

Finally, a prior must be specified for the random effects. By definition of the log-Normal frailty model, it is assumed that the u_j 's follow a Normal distribution with mean zero and variance σ_u^2 . In WinBUGS, the variance is specified in terms of the precision, τ ; therefore, the prior distribution for the u_j 's is

$$u_j \sim \text{Normal}(0, \tau) , (j = 1, \dots, 624).$$

A hyperprior must also be specified for the variance term. A vague hyperprior will also be used for this. There are a couple of options usually adopted by WinBUGS for this purpose. The first option is a vague Uniform prior on the standard deviation, and the second option is a vague Gamma prior on the precision i.e. an inverse-Gamma prior on the variance. The WinBUGS manual advises the use of the Uniform prior on the standard deviation with use of the Gamma prior on the precision generally not recommended as it can commonly cause trap messages [245]. Gustafson [231] also discussed why an inverse-Gamma prior on the variance may not be appropriate.

Therefore, the following vague hyperprior was specified for the random effects standard deviation:

$$\sigma_u \sim \text{Uniform}(0, 1).$$

Lambert et al. [246] recommended that a sensitivity analysis should be performed when using prior distributions that are intended to be vague for the between-unit variance. However, they also discussed how the influence of the prior distribution is reduced as the number of higher-level units increases. As there are a large number of postcode sectors in the SHeS dataset (624 postcode sectors), inferences should not be sensitive to the choice of prior distribution for this parameter.

7.4.5 Estimating the Parameters in WinBUGS

7.4.5.1 Markov Chain Monte Carlo

Bayesian Markov chain Monte Carlo (MCMC) methods are commonly used as estimation procedures in shared frailty models. The posterior distribution in hierarchical models, such as the frailty model, is usually difficult to integrate out in order to find the marginal posterior of each random parameter [225]; however, MCMC methods can now allow analysis based on previously intractable posterior distributions [231]. MCMC methods avoid the need for high-dimensional integration by performing the integration implicitly through generating samples from the joint posterior distribution of the unknown parameters [247, 248].

The general idea behind MCMC is as follows. Suppose the target distribution, $\pi(\theta)$ for $\theta \in E \subset \mathbf{R}^n$, where $\pi(\theta) = p(\theta | x)$ (the posterior distribution) is complex and cannot be sampled from directly. Samples from π can, however, be obtained indirectly by constructing a Markov chain with state space E whose equilibrium (stationary) distribution is $\pi(\theta)$. If the chain is run for long enough, simulated values can thus be treated as a dependent sample from the target (posterior) distribution which can be used to summarise characteristics of π . In order to reach the stationary distribution, the chain must satisfy three conditions. It must be irreducible, aperiodic and positive recurrent. Further details of this can be found in Gilks et al. [249].

Markov chains with the desired stationary distribution are constructed using MCMC algorithms, the two most common being the Gibbs sampler and the Metropolis-Hastings algorithm. The Gibbs sampler is the easiest algorithm to implement and is the algorithm adopted by WinBUGS. Therefore, only Gibbs sampling will be discussed in this thesis (Section 7.4.5.2). However, details of the Metropolis-Hastings algorithm can be found in Smith & Roberts [250], Brooks & Roberts [251], Gilks et al. [249] and Gamerman & Lopes [210].

7.4.5.2 Gibbs Sampling

This subsection will give a brief introduction to Gibbs sampling. For a more comprehensive review refer to Gilks et al. [249] and Gamerman and Lopes [210].

The Gibbs sampler is an iterative Monte Carlo method used to generate samples from difficult multivariate posterior distributions. It generates samples indirectly from the joint distribution of the parameters without having to calculate the density by repeatedly sampling from the full conditional posterior distributions of the model parameters to produce realisations from the joint posterior distribution. Considering only one unknown quantity at a time, the Gibbs sampler generates a value from the corresponding full conditional distribution given the current values of the other quantities [230]. In general, the Gibbs sampler proceeds as follows. Suppose the parameter θ is partitioned into p subvectors (or possibly scalars) such that

$$\theta = \{ \theta_1, \theta_2, \dots, \theta_p \}.$$

If the current state of the Markov chain is

$$\theta^{(t)} = \{ \theta_1^{(t)}, \theta_2^{(t)}, \dots, \theta_p^{(t)} \},$$

then the Gibbs sampler proceeds to $\theta^{(t+1)}$ in p steps as follows.

1. Sample $\theta_1^{(t+1)}$ from $\pi(\theta_1 \mid \theta_2^{(t)}, \dots, \theta_p^{(t)})$
2. Sample $\theta_2^{(t+1)}$ from $\pi(\theta_2 \mid \theta_1^{(t+1)}, \theta_3^{(t)}, \dots, \theta_p^{(t)})$
- ...
- p. Sample $\theta_p^{(t+1)}$ from $\pi(\theta_p \mid \theta_1^{(t+1)}, \dots, \theta_{p-1}^{(t+1)})$.

This process generates a Markov chain and, provided each conditional distribution is sampled from sufficiently frequently, under a wide set of conditions, the samples obtained are from the joint posterior distribution, where $\theta^{(t)}$ is the state vector of a convergent Markov chain with the posterior distribution as the stationary distribution [252]. Samples obtained from the posterior distribution can then be used for inference.

Gilks et al. [249] considered some steps required to implement Gibbs sampling. Firstly, they stated that starting values must be provided for all unobserved nodes. Starting, or ‘initial’ values, as they are referred to in WinBUGS and will be referred to in the thesis from here on, are chosen for the parameters of the model before proceeding through the steps of the algorithm. Although WinBUGS can generate initial values for unobserved nodes by forward sampling from the prior distribution for each parameter [245], it is recommended that initial values should be provided for parameters with vague prior distributions. The values chosen for initial values are not particularly important in terms of inferences made from Gibbs sampling since, when the chain is run for long enough to achieve equilibrium, it loses all dependence on initial values [247, 249]. However, choice of initial values can affect the performance of the chain, for example, the speed at which it reaches convergence. Methods adopted for the selection of initial values have included, for example, using estimates from simpler models by setting the hyperparameters to fixed values, or, alternatively, using maximum likelihood estimates [247, 253]. More rigorous methods of selection of initial values are discussed in Brooks [247] and references therein.

Construction of the full conditional distributions for each unobserved node is the second point to be considered by Gilks et al. [249]. The full conditional distributions are derived from the joint distribution of the variables as follows.

$$\pi(\theta_i | \theta_{-i}) = \frac{\pi(\theta_i, \theta_{-i})}{\int \pi(\theta_i, \theta_{-i}) d\theta_i} .$$

WinBUGS automatically constructs the full conditional distributions and chooses appropriate methods for sampling from them [254]. If random variables are Gamma, inverse-Gamma or Normally distributed, as is usually the case in frailty models, sampling is fairly straightforward via standard algorithms. However, in other cases, alternative random variate generating methods, such as the ‘inversion method’ or the ‘rejection method’, can be used [213]. If the full conditional posterior distributions of the model parameters can be shown to be log-concave, adaptive rejection sampling can be used. See Dellaportas and Smith [213] for a definition of log-concavity, and Dellaportas and Smith and Gilks et al.

[249] for a discussion of adaptive rejection sampling as well as alternative methods for random variate generation.

The third point considered by Gilks et al. [249] is that of monitoring convergence. This issue will be discussed separately in Section 7.4.6.

7.4.6 Monitoring Convergence in WinBUGS

Section 7.4.5 above discussed that, provided a Markov chain is run for long enough during a period referred to as ‘burn-in’, simulated values can be treated as a dependent sample from the target (posterior) distribution which can be used to summarise characteristics of π . The purpose of the burn-in period is to remove dependence of the simulated chain on its starting location [253] in order for effective convergence to be reached. One of the main problems, however, is determining the length of the burn-in period in order to safely assume that all further samples are representative of the stationary distribution of the Markov chain. Therefore, it is necessary to assess convergence using procedures called ‘convergence diagnostics’.

The study of convergence can be approached in two ways. The first approach is theoretical and will not be considered here. However, a discussion of this can be found in Cowles & Carlin [255] and Gamerman & Lopes [210] and references therein. The second approach applies diagnostic tools to the output of the simulation, and will be the approach considered here. Cowles & Carlin recommended that a variety of diagnostic tools should be used to assess convergence, and there are a number available in WinBUGS. In particular, convergence will be assessed here by using the Gelman-Rubin method and trace plots for each parameter. These will be reviewed in Sections 7.4.6.1 and 7.4.6.2 below. However, comprehensive reviews of further techniques for monitoring convergence can be found in Cowles & Carlin, Brooks & Roberts [251], Gilks et al. [249] and Gamerman & Lopes [210].

7.4.6.1 Gelman-Rubin Method

The method proposed by Gelman & Rubin [256] requires that m chains, each of length $2n$, where the first n iterations are discarded to avoid the burn-in period, are simulated in parallel. All the chains should have different starting points which are overdispersed in terms of the target distribution. In short, it is based on a comparison of the within and between chain variance for each variable [225].

Suppose $\theta(x)$ represents some scalar function of interest, and has mean μ and variance σ^2 under the target distribution, π . The degree of information about θ can be represented by $1/\sigma^2$ [251].

The method supposes that if $\hat{\mu}$ is an unbiased estimator of μ and $\hat{\sigma}^2$ provides an estimate of σ^2 from the sample output, then

$$R = \frac{\hat{V}}{\sigma^2}$$

where R is known as the scale reduction factor (SRF), will be an estimate of the proportion of the total amount of information available about θ that has been obtained from the simulations used to construct \hat{V} [251]. \hat{V} provides a pooled posterior variance estimate by accounting for the sampling variability of the estimators $\hat{\mu}$ and $\hat{\sigma}^2$ and is written as

$$\hat{V} = \hat{\sigma}^2 + B/mn,$$

where B/n is the variance between the m sequence means as defined below.

However, firstly $\hat{\sigma}^2$, a weighted average of the between and within chain variance estimators, must be calculated as follows.

To begin, define B/n as the variance between the m sequence means, $\bar{\theta}_{i.}$, each based on n values of θ where

$$\frac{B}{n} = \frac{\sum_i (\bar{\theta}_{i.} - \bar{\theta}_{..})^2}{(m-1)}, \quad (i = 1, \dots, m)$$

Next, W , the average of the m within-sequence variances, s_i^2 , each of which has $n-1$ degrees of freedom, is defined as

$$W = \sum_i s_i^2 / m, \quad (i = 1, \dots, m).$$

$\hat{\sigma}^2$ is thus calculated as

$$\hat{\sigma}^2 = \frac{n-1}{n} W + \frac{1}{n} B.$$

Under stationarity, $\hat{\sigma}^2$ is an unbiased estimator of σ^2 , but will overestimate σ^2 if the starting distribution is appropriately overdispersed. Brooks & Gelman [257] warn that $\hat{\sigma}^2$ can be too low if over-dispersion does not hold, meaning that convergence can be falsely diagnosed.

Following calculation of $\hat{\sigma}^2$, \hat{V} and hence R , the scale reduction factor, can be calculated. However, the denominator of R , σ^2 , is unknown, and therefore it must be estimated from the data. W is thus used to provide an (under)estimate of σ^2 , which, in turn, means R can be (over)estimated by

$$\hat{R} = \frac{\hat{V}}{W} = \frac{m+1}{m} \frac{\hat{\sigma}^2}{W} - \frac{n-1}{mn}.$$

\hat{R} is referred to as the potential scale reduction factor (PSRF) and can be interpreted as a convergence diagnostic. If the value of \hat{R} is large, then $\hat{\sigma}^2$ can be decreased further by running more simulations, thereby improving inference about the target distribution, as it is clear that the simulated sequences have not yet made a full tour of the target distribution [257]. However, if \hat{R} is close to 1, then it can be concluded that each of the m sets of n simulated observations is close to the target distribution [257].

The PSRF can be modified to account for sampling variability in the variance estimates by using the correction factor $(d+3)/(d+1)$. Justification of this correction factor can be found in Gelman & Rubin [256] and Brooks & Gelman [257].

Using this correction factor gives the corrected scale reduction factor (CSRF), which is defined as

$$\hat{R}_c = \frac{(d+3)}{(d+1)} \hat{R} = \frac{(d+3)}{(d+1)} \frac{\hat{V}}{W} .$$

Interpretation of \hat{R}_c is the same as that for \hat{R} . It is usually taken to assume that convergence has been reached if $\hat{R}_c < 1.2$ for all parameters [257].

This original method was further developed by Brooks & Gelman [257] so that more than one parameter could be considered simultaneously. In that case, θ denotes a vector of parameters. Further details of this can be found in Brooks & Gelman and Brooks & Roberts [251].

The CSRF provides a useful indicator as to whether or not convergence has been attained; however, Brooks & Gelman [257] argued that monitoring \hat{R}_c alone only considers one of the three conditions which should hold at convergence. At convergence, as well as \hat{R}_c approaching 1, the other conditions to hold are that the mixture-of-sequences variance, V , should stabilise as a function of n and the within-sequence variance, W , should stabilise as a function of n [257]. They considered an alternative graphical approach to monitoring convergence by dividing the m sequences into batches of length b , and then calculating $V(k)$, $W(k)$ and $\hat{R}_c(k)$ based on the second half of the observations of a sequence of length $2kb$ ($k = 1, \dots, n/b$) for some suitably large n [257]. Then, as well as plotting $\hat{R}_c(k)$ against k , the two scale factors, $V^{1/2}(k)$ and $W^{1/2}(k)$, functions of k can be included on the same plot. Both plots stabilising at the same value indicates that convergence has been attained. Brooks & Gelman [257] noted that the scale factors are given to the power $1/2$ in order to be on a directly interpretable scale.

WinBUGS allows $\hat{R}_c(k)$ and the two scale factors to be plotted together. A red line is used to indicate $\hat{R}_c(k)$, a green line indicates the width of the central 80% interval of the pooled runs, and a blue line indicates the average width of the 80% intervals within the individual runs [245]. As discussed above, convergence is attained when \hat{R}_c (red line) approaches 1 and the pooled and within interval widths (green and blue lines respectively) stabilise at the same value. Spiegelhalter et al. [245] noted that the pooled and within-interval widths are normalised to have an overall maximum of one for plotting purposes. These plots will be used to monitor convergence when fitting the frailty models along with trace plots for each parameter. Refer to Section 7.4.6.2 for a discussion of trace plots.

Although the Gelman-Rubin method requires multiple sequences to be run in parallel using a range of different starting values, Jackman [252] noted that some authors prefer one long run of a MCMC sampler rather than several shorter ones, especially in a situation where convergence is slow (refer to Brooks [247] for a further discussion). However, given improvements in computational power, it is now usually recommended that ‘more is better’ [252]. Indeed, there are a number of advantages in running multiple chains, as problems that would otherwise not be revealed if only one chain was being run, such as poor mixing, can be revealed [253].

7.4.6.2 Trace Plots

As discussed previously, Cowles & Carlin [255] recommended that a variety of diagnostic tools should be used to assess convergence. In addition to more formal techniques, such as the Gelman-Rubin method, ‘trace plots’ may also be used to assess convergence for each parameter of interest. Trace plots, which are easily attained in WinBUGS, display the iterative history of MCMC sequences by plotting the sample values versus iteration number to try and assess when the simulation appears to have stabilised. If running only one chain, on graphical inspection the chain should be fairly stable around a sample value, and the trace should be ‘caterpillar-like’ in appearance if convergence is reasonable. If more

than one chain is being run simultaneously, in addition to the conditions which indicate convergence when only one chain is run, the multiple chains, which WinBUGS plots in different colours, should be overlapping each other. If this is not the case, and the chains do not appear to be ‘mixing’ well, where mixing refers to the degree to which a simulated chain spans the entire parameter space [253], then a bigger burn-in period may be required.

7.4.6.3 Iterations After Convergence

Once convergence has been attained, it is necessary to run the simulation for further iterations in order to obtain the samples to be used for posterior inference. Although the accuracy of the posterior estimates will improve as the number of samples saved increases, running too many further iterations will not be computationally efficient. Therefore, Spiegelhalter et al. [245] have suggested a way in which the accuracy of the posterior estimates may be assessed. For each parameter, this is done by calculating an estimate of the difference between the mean of the sampled values, which is being used as an estimate of the posterior mean, and the true posterior mean to give what is referred to as the ‘Monte Carlo error’ (MC error).

Spiegelhalter et al. [245] recommended that, as a rule of thumb, the simulation should be run until the Monte Carlo error for each parameter of interest is less than around 5% of the sample standard deviation (SD). Both the MC error and SD are reported in the summary statistics table produced by WinBUGS.

8 Fitting Alternative Methods to the Scottish Dataset: Results

This section presents results obtained from fitting the three methods described in Chapter 7 to the Scottish Health Survey dataset.

8.1 Defining Different Risk Sets

The first alternative to be considered involved defining different risk sets. Instead of having a risk set for each failure time as in continuous-time hazard models, which, in the context of the Scottish Health Survey data, was the time at which an individual was admitted to psychiatric facilities as measured in days from survey interview, the time scale is divided into short intervals, and failures are observed within each interval. As reviewed in Section 7.2, the data were expanded so that each individual had a line of data corresponding to each risk set they survived. Discrete-time hazard models were fitted with a binary response coded as 1 if an individual was admitted to psychiatric facilities in the time period, and 0 otherwise. Censoring was as in the continuous-time hazard models (Section 5.4.1). As individuals were nested within postcode sectors, a random effect for postcode sector was incorporated into the model to account for the hierarchical structure.

For both the 1995 and 1998 surveys, follow-up time was measured from the date of survey interview until 2004. Instead of treating time as continuous and observing it in days, it may also seem natural to group follow-up time into years. Grouping time into yearly intervals implied that there were fewer risk sets and hence the size of the expanded dataset was reduced. Although grouping time into yearly intervals led to a reduction in the size of the expanded dataset, it was also of interest to investigate whether it was possible to establish a more effective way of grouping time in order to reduce the size of the expanded dataset further. To do this, time intervals were defined so that they corresponded to times when events occurred, and thus the length of each discrete time interval varied. The time intervals were constructed in such a way

that the size of the expanded dataset was reduced as much as possible with a minimal loss of information.

Sections 8.1.1 and 8.1.2 present results obtained from fitting two-level discrete-time hazard models in MLwiN for when time intervals were grouped into years and were of varying length respectively. Models were re-run including all available risk factors in order to investigate if significant variables and parameter estimates in the final discrete-time hazard models were comparable to those obtained when fitting continuous-time hazard models (Section 5.4). The modelling strategy employed when fitting the discrete-time hazard models was identical to that when fitting the continuous-time models in that three separate models were fitted. To recap, the three models included a model with GHQ-12 score only as a way of investigating the association between GHQ-12 score and the hazard of first psychiatric admission, a model adjusting for all significant risk factors apart from self-assessed general health and, finally, a model adjusting for all significant risk factors including self-assessed general health as a potential risk factor. For further information on the modelling strategy see Section 5.4.1, and for further information on the relationship between GHQ-12 score and self-assessed general health see Section 3.2.1.2.

8.1.1 Multilevel Discrete-Time Models with Equal Intervals of Time

Table 8.2 displays results obtained from fitting discrete-time hazard models with year-long time intervals. In order to make results obtained from fitting discrete-time hazard models comparable with results obtained from fitting the continuous-time hazard models (Table 5.3), first-order PQL was used to estimate the parameters. A discussion of estimation procedures in MLwiN for non-linear models can be found in Section 5.3.5. It should be noted again that results are for those respondents with no psychiatric admissions prior to survey interview.

The last observation (which was censored) occurred at 3476 days from survey interview suggesting ten year-long intervals; however, as the last event (admission) occurred at 3046 days from survey interview, the data were restructured into nine risk sets, with all ‘survivors’ being censored after this

time. An example of the expanded dataset obtained in MLwiN for the first individual is displayed in Table 8.1 below.

Table 8.1 - Expanded dataset with equal discrete time intervals

ID	Response	Failure	Risk Set Indicator	Survival Time	Number at Risk
1	0	25	1	1	15208
1	0	24	2	2	15093
1	0	19	3	3	14971
1	0	23	4	4	14846
1	0	16	5	5	14453
1	0	16	6	6	6974
1	0	8	7	7	6924
1	0	4	8	8	6860
1	0	2	9	9	550
.
.
.

Size of dataset = 110643

As shown in Table 8.1, grouping time into year-long intervals reduced the size of the expanded continuous-time dataset (Table 5.2) from just fewer than 1.9 million observations within individuals to just fewer than 111000 observations within subjects. This was a reduction of approximately ninety four percent.

A two-level discrete-time model with a fourth-order polynomial describing the underlying hazard was fitted in MLwiN. The logit link was used to model the hazard. Note that results obtained here will be compared with results obtained from fitting the continuous-time proportional hazards models (models B1, B2 and B3) displayed in Table 5.3.

Table 8.2 - Results from ML discrete-time models with equal intervals

	Model C1 Estimate(s.e)	Model C2 Estimate(s.e)	Model C3 Estimate(s.e)
<i>Fixed</i>			
Intercept (β_0)	-7.059(0.911)	-7.536(0.939)	-7.667(0.943)
t_{ij} (α_1)	0.214(1.188)	0.154(0.170)	0.056(1.170)
t_{ij}^2 (α_2)	-0.147(0.484)	-0.117(0.476)	-0.071(0.476)
t_{ij}^3 (α_3)	0.029(0.076)	0.024(0.075)	0.016(0.075)
t_{ij}^4 (α_4)	-0.002(0.004)	-0.002(0.004)	-0.001(0.004)
GHQ-12 Score			
0	0.000**	0.000**	0.000*
1-2 (β_1)	0.698(0.226)	0.571(0.227)	0.482(0.229)
3-4 (β_2)	0.962(0.278)	0.674(0.282)	0.530(0.286)
5-12 (β_3)	1.351(0.218)	0.943(0.226)	0.707(0.236)
Sex			
Male		0.000	0.000
Female (β_4)		-0.145(0.186)	-0.105(0.187)
Age			
16-24		0.000	0.000
25-34 (β_5)		-0.276(0.286)	-0.246(0.287)
35-44 (β_6)		0.005(0.277)	0.044(0.279)
45-54 (β_7)		-0.642(0.333)	-0.694(0.335)
55-64 (β_8)		-0.210(0.303)	-0.318(0.308)
65-74 (β_9)		0.123(0.385)	0.162(0.387)
Marital Status			
Married/cohabiting		0.000	0.000
Other (β_{10})		0.478(0.179)	0.395(0.181)
Receipts of Benefits			
No		0.000	0.000
Yes (β_{11})		0.799(0.200)	0.600(0.209)
Smoking Status			
Non-Smoker		0.000	0.000
Current Smoker (β_{12})		0.810(0.213)	0.718(0.215)
Ex-Smoker (β_{13})		0.036(0.300)	0.016(0.301)
Employment Status			
Full-Time		0.000	0.000
Unemployed (β_{14})		0.427(0.262)	0.545(0.267)
Part-Time (β_{15})		-0.364(0.253)	-0.315(0.254)
Self-Assessed Health			
Very Good			0.000
Good (β_{16})			0.512(0.225)
Fair (β_{17})			0.973(0.250)
Bad (β_{18})			0.206(0.552)
Very Bad (β_{19})			1.932(0.457)

Random

Area Variation(σ_u^2)	0.245(0.263)	0.191(0.249)	0.233(0.246)
ICC	0.069	0.055	0.066

* $p_{\text{trend}} < 0.05$

** $p_{\text{trend}} < 0.001$

Model C1 demonstrated a highly significant increasing trend in the hazard of first psychiatric admission following survey interview ($p < 0.001$) as GHQ-12 score increased. Taking the anti-logit of the intercept revealed that, after adjusting for GHQ-12, the probability of psychiatric admission in the average postcode sector was 0.000859. The intraclass correlation (ICC = 0.069) indicated that 6.9% of the total variation was attributable to the level of postcode sector. Parameter estimates obtained for the fixed effects in model C1 were very similar to those obtained in model B1. There were slight differences in the estimates of the random effects between models C1 and B1. The postcode sector variation was underestimated using the discrete-time model (C1) compared to the Poisson model (B1). However, when fitting discrete-time models the response follows a Binomial distribution, as opposed to continuous-time models where the response is Poisson-distributed. As a result, these models and hence parameter estimates, are not strictly comparable. It can be observed, however, that the 95% confidence interval (not displayed here) for the higher-level variance in model B1 contained the value of the estimate obtained in model C1.

Model C2 allowed for the adjustment of all significant risk factors apart from self-assessed general health. The increasing trend in the hazard of admission as GHQ-12 score increased remained highly significant following adjustment for all significant risk factors. In addition to having a GHQ-12 score of 1 or more, other significant risk factors associated with an increased hazard of admission included not being married (i.e. single, separated, divorced or widowed), being in receipt of benefits and being a current smoker. Neither of the area-level risk factors was significantly associated with the outcome, and thus model C2 contained individual-level risk factors only. The intraclass correlation decreased to 5.5% as a result of adjusting for further significant demographic, socioeconomic and lifestyle risk factors, with 22% of the total unexplained variation between

postcode sectors being attributed to going from model C1 to model C2. Model C2 is identical to model B2 in terms of risk factors significantly associated with an increased hazard of psychiatric admission. Comparing model C2 to model B2 also revealed that the parameter estimates obtained for the fixed effects were very similar for the two models. However, the postcode sector variation was underestimated. Reasons for this difference were discussed above.

The final model (model C3) allowed for adjustment of all significant risk factors including self-assessed general health. As in previous models (A3 and B3), the relationship between GHQ-12 score and psychiatric admission was attenuated following the inclusion of self-assessed general health; however, the increasing trend in the hazard of psychiatric admission remained significant. Parameter estimates for the fixed and random effects in model C3 were comparable to those obtained in model B3, with the same risk factors being associated with an increased hazard of psychiatric admission in the two models. In addition to a GHQ-12 score of one or more, these included not being married (i.e. single, separated, divorced or widowed), being in receipt of benefits, being a current smoker, being unemployed and having a self-assessed general health rating other than 'very good' (i.e. 'good', 'fair', 'bad' or 'very bad'). As in model B3, the between-postcode sector variation in model C3 ($\sigma_u^2 = 0.233$) had increased as a result of including self-assessed general health in the model; however, the discrete-time model was still underestimating this parameter.

8.1.2 Multilevel Discrete-Time Models with Varied Intervals of Time

It was discussed above that time intervals should be constructed in such a way as to reduce the size of the expanded dataset to the greatest extent possible whilst retaining as much information as possible. Therefore, as an alternative to fitting strict year-long time intervals, the lengths of the intervals were allowed to vary according to when admissions occurred. Time was divided into five intervals which were defined as shown in Table 8.3 below.

Table 8.3 - Groupings for varying discrete time intervals

Time Interval	Day
1	0 – 400
2	401 – 1620
3	1621 – 2063
4	2064 – 3046
5	3047 - 3476

Since the last event (admission) occurred at 3046 days from survey interview, the last time interval, which ranges from 3047 to 3476 days from survey interview consists of ‘survivors’ only. These observations were censored during this interval. Since the last time interval included only censored observations, it was not included as a risk set in the person-period dataset. Table 8.4 below presents the expanded dataset for the first individual when risk sets were defined as shown in Table 8.3.

Table 8.4 - Expanded dataset with varying discrete time intervals

ID	Response	Failure	Risk Set Indicator	Survival Time	Number at Risk
1	0	26	1	1	15192
1	0	73	2	2	14794
1	0	21	3	3	9289
1	0	17	4	4	5023
.
.
.

Size of dataset = 54580

Table 8.4 demonstrates that the size of the person-period dataset was reduced further when lengths of time intervals were allowed to vary between risk sets. Defining risk sets according to when admissions occurred reduced the size of the dataset to fewer than 55000 observations within individuals. This was a 97% reduction on the continuous-time person-period dataset (Table 5.2), and a

reduction of more than half (51%) on the expanded dataset when time was grouped into year-long intervals (Table 8.1).

A two-level discrete-time model using a logit link to model the hazard was fitted in MLwiN. As there were only four risk sets, dummy variables known as ‘blocking factors’ were used for the modelled time intervals, with the first risk set being taken as the baseline. As in models C1, C2 and C3 above, results obtained here were compared with those obtained from fitting continuous-time hazard models (models B1, B2 B3) as displayed in Table 5.3.

Results from model D1 indicated a highly significant increasing trend in the hazard of first psychiatric admission during follow-up as GHQ-12 score increased ($p < 0.001$). Parameter estimates obtained for the fixed effects (GHQ-12 score) were very similar to those obtained in model B1 and also in model C1. However, postcode sector variation in model D1 ($\sigma_u^2 = 0.279$) was slightly larger than in models B1 and C1 which had estimates of $\sigma_u^2 = 0.255$ and $\sigma_u^2 = 0.245$ respectively. This may be a consequence of the widths of the longer time intervals. When there are fewer risk sets as a result of having wider discrete-time intervals, it is more likely that the hazard of event for individuals within a postcode sector will be similar, i.e. that more individuals in that postcode sector to be admitted in each risk set (given that they have already survived until that time). If there is less variation (between individuals) within a higher-level unit, then this implies more variation between the higher-level units. This could explain why the estimate of the random effects variance is higher in model D1 than in B1 and C1. However, it should be noted that the 95% confidence interval for the random effects variance (not displayed here) obtained from fitting the continuous-time model, model B1, does in fact contain the value of the estimate obtained in model D1.

Table 8.5 - Results from ML discrete-time models with varying intervals

	Model D1 Estimate(s.e)	Model D2 Estimate(s.e)	Model D3 Estimate(s.e)
Fixed			
Intercept (β_0)	-6.927(0.232)	-7.435(0.357)	-7.634(0.372)
t2 _{ij} (α_1)	1.047(0.229)	1.056(0.229)	1.062(0.229)
t3 _{ij} (α_2)	-0.169(0.294)	-0.149(0.294)	-0.139(0.294)
t4 _{ij} (α_3)	0.081(0.313)	0.071(0.314)	0.016(0.314)
GHQ-12 Score			
0	0.000**	0.000**	0.000*
1-2 (β_1)	0.699(0.227)	0.574(0.228)	0.482(0.230)
3-4 (β_2)	0.963(0.279)	0.677(0.283)	0.531(0.288)
5-12 (β_3)	1.350(0.219)	0.940(0.228)	0.697(0.237)
Sex			
Male		0.000	0.000
Female (β_4)		-0.140(0.187)	-0.098(0.188)
Age			
16-24		0.000	0.000
25-34 (β_5)		-0.280(0.287)	-0.249(0.288)
35-44 (β_6)		0.004(0.278)	0.043(0.280)
45-54 (β_7)		-0.657(0.334)	-0.710(0.337)
55-64 (β_8)		-0.227(0.305)	-0.341(0.310)
65-74 (β_9)		0.060(0.386)	0.100(0.388)
Marital Status			
Married/cohabiting		0.000	0.000
Other (β_{10})		0.494(0.180)	0.406(0.182)
Receipts of Benefits			
No		0.000	0.000
Yes (β_{11})		0.796(0.201)	0.591(0.210)
Smoking Status			
Non-Smoker		0.000	0.000
Current Smoker (β_{12})		0.803(0.214)	0.719(0.216)
Ex-Smoker (β_{13})		0.034(0.301)	0.013(0.302)
Employment Status			
Full-Time		0.000	0.000
Unemployed (β_{14})		0.433(0.266)	0.557(0.269)
Part-Time (β_{15})		-0.360(0.254)	-0.309(0.255)
Self-Assessed Health			
Very Good			0.000
Good (β_{16})			0.530(0.225)
Fair (β_{17})			0.997(0.251)
Bad (β_{18})			0.244(0.555)
Very Bad (β_{19})			1.986(0.462)
Random			
Area Variation(σ_u^2)	0.279(0.266)	0.223(0.254)	0.257(0.251)
ICC	0.078	0.064	0.072

Model D2 was fitted as in model B2, with self-assessed general health being excluded as a possible risk factor. Once again, the increasing trend in the hazard of psychiatric admission remained highly significant following adjustment for all significant risk factors, apart from self-assessed general health. Risk factors selected in model D2 as being significantly associated with an increased hazard of psychiatric admission were exactly as in model B2 (and C2), with parameter estimates for the fixed effects being very similar to those in model B2 (and C2). The postcode sector variation in model D2 ($\sigma_u^2 = 0.223$) was again slightly higher than in models B2 and C2, where the postcode sector variation was $\sigma_u^2 = 0.201$ and $\sigma_u^2 = 0.191$ respectively. A similar argument to that discussed for model D1 applies here also.

Finally, self-assessed general health was permitted to be included as a potential risk factor, with model D3 displaying all significant risk-factors in Table 8.5 above. Parameter estimates for the fixed effects were once again similar to those in model B3 (and C3). The postcode sector variation in model D3 ($\sigma_u^2 = 0.257$) was slightly higher than in model B3 ($\sigma_u^2 = 0.246$) and model C3 ($\sigma_u^2 = 0.233$). Again, the argument justifying the larger higher-level variance in model D1 compared to B1 and C1 can be applied here. As in models B3 and C3, the postcode sector variation in model D3 increased as a result of adding self-assessed general health to the model.

8.1.3 Summary: Defining Different Risk Sets

As an alternative to fitting multilevel continuous-time hazard models, which can lead to a vast increase in the size of the original dataset following expansion, this section investigated ways in which different risk sets could be defined to reduce the size of the expanded person-period dataset with minimal loss of information. This involved grouping time into short intervals and fitting multilevel discrete-time hazard models. Two possible groupings of time were considered. The first involved grouping time into year-long intervals so that each risk set was the same length. The second allowed the size of each risk set to vary, with time intervals defined corresponding to when events occurred.

The effectiveness of these methods at reducing the size of the expanded dataset was tested through their application to the Scottish Health Survey dataset. Grouping time into year long intervals led to a 94% reduction of the size of expanded dataset in the continuous-time case, where each day at which an event occurred was defined as a risk set. This percentage was increased further when risk sets were allowed to vary in size. The reductions achieved were 97% in the continuous-time person-period dataset and 51% in the discrete-time person-period dataset with year-long intervals.

Comparing results from both discrete-time models in Tables 8.2 and 8.5 with the continuous-time models (Table 5.3) revealed that significant risk factors associated with first psychiatric admission during follow-up were the same across all three models, with parameter estimates for the fixed and random effects being very similar also. As results across the three sets of models were comparable, this suggested that discrete-time hazard models could be used as an alternative to fitting continuous-time hazard models. Discrete-time models can lead to a vast reduction in the size of the expanded dataset, and therefore allow models to be estimated more efficiently.

8.2 Grouping According to Covariates

The second method to be considered as an alternative to fitting continuous-time proportional hazards models involved grouping according to covariates. This method entailed grouping all individuals in the same postcode sector with the same values for covariates being fitted in a particular model and creating one line of data for these individuals as opposed to having a line of data for each individual. The concept behind this method is that all individuals within the same postcode sector with the same values for covariates included in a particular model are at risk at the same time. Therefore, they can be represented by one line of data meaning that the size of the person-period dataset can be reduced. When individuals were aggregated according to their characteristics there was a slight change in the nesting structure. In the case of the SHeS dataset there were still two levels, with postcode sectors remaining at

the higher-level (level-2). However, at level-1 there was a new pseudo-level of cells defined by each possible combination of the chosen characteristics. A further description of this method and the algebraic derivation was given in Section 7.3.

The grouping according to covariates method was applied to both continuous-time and discrete-time models. For the continuous-time models, each risk set represented a particular day on which a psychiatric admission occurred, as was the case with the original continuous-time models in Section 5.4. The response became the number of individuals from the same postcode sector with the same values for covariates in a particular model who were admitted to psychiatric facilities in a particular risk set. In the discrete-time case, risk sets represented defined intervals corresponding to when events occurred, and therefore the intervals varied in length. The response for the discrete-time models was the proportion of individuals from the same postcode sector with the same values for covariates in a particular model who were admitted to psychiatric facilities in a particular risk set. For both types of model, observations were censored if the subject died or reached the end of follow-up without experiencing a psychiatric admission.

Section 8.2.1 presents results obtained from fitting both continuous- and discrete-time models for the grouping according covariates method. Three models were fitted: the first with GHQ-12 score only; the second with GHQ-12 score, age and sex and finally, the fully adjusted model including self-assessed general health. A new grouped dataset had to be created each time a new model was fitted as the number of individuals within each cell at level-1 changed as covariates were added or removed from the model since cell definition changes as covariates are added or removed from the model. For example, if the model contained the variable 'sex' only, then cells are defined by sex, i.e. there would be a cell for both males and females nested within each level-2 unit. However, if the model contained 'sex' and 'age', there would then be a cell for every possible combination of sex and age.

Results obtained from fitting the continuous-time and discrete-time models for this method are shown in Tables 8.7 and 8.10 below. Parameters were estimated using first-order PQL in order to make results comparable with the other

methods presented in this chapter. As with all other analyses in this chapter, results are for those with no psychiatric admissions prior to survey interview.

8.2.1 Results from Grouping According to Covariates in Continuous Time

The aggregated datasets were derived from the original continuous-time expanded person-period dataset (Table 5.2). Table 8.6 below shows the expanded dataset for the first postcode sector when the data were grouped according to GHQ-12 score, i.e. each level 1 ‘cell’ corresponded to a particular GHQ-12 score nested within postcode sectors.

When grouping on GHQ-12 score, nested within each postcode sector, there were 4 pseudo-level-1 cells. These corresponded to each of the four categories of GHQ-12 score (i.e. score 0, score 1-2, score 3-4, score 5-12), as indicated by the ‘cell ID’ column. If any of the cells were empty, i.e. there was no individual within a particular postcode sector with a particular category of GHQ-12 score, this cell could be omitted. Each cell within a postcode sector then had a line of data corresponding to each risk set. In the dataset there were 136 distinct failure times and, as time was being treated as continuous here also, this meant that there was a risk set corresponding to each distinct failure time, implying that there were 136 risk sets. The ‘no. at risk in cell’ column indicates how many individuals there were within each cell nested within postcode sector at risk at the beginning of each risk set.

For cell ID 1, Table 8.6 indicates that there were 10 individuals at risk in the first risk set, i.e. 10 individuals within this postcode sector had GHQ-12 score 0. As no individual in this cell ‘failed’ (indicated by the ‘no. of failures in cell’ column) or was censored, there continued to be 10 individuals at risk in the last risk set. The ‘no. of total individual failures’ column indicates the total number of individuals who failed within the whole dataset overall - it is not specific to cells or postcode sectors. This column and the ‘no. at risk in cell’ column were required to form the offset for the continuous-time Poisson model being fitted to the aggregated dataset.

Table 8.6 - Expanded dataset when grouping according to GHQ-12 score in continuous-time

Postcode Sector	Cell ID	GHQ-12 Score	Risk Set Indicator	No. at Risk in Cell	No. of Failures in Cell	No. of Total Individual Failures	Survival Time (days)
95001	1	0	1	10	0	1	20
95001	1	0	2	10	0	1	40
.
.
95001	1	0	136	10	0	1	3046
95001	2	1-2	1	7	0	1	20
.
.
95001	2	1 – 2	136	7	0	1	3046
95001	3	3 – 4	1	1	0	1	20
.
.
95001	3	3 – 4	136	1	0	1	3046
95001	4	5 – 12	1	3	0	1	20
.
.
95001	4	5 - 12	136	2	0	1	3046

Size of dataset = 298172

Table 8.6 also revealed that aggregating the data in this way (grouped on GHQ-12 score only) reduced the size of the expanded person-period dataset by around 84%; from just fewer than 1.9 million observations within individuals in the original continuous-time expanded dataset (Table 5.2) to just fewer than 300000 observations (cells). Although this was a good reduction, it was presumed that this percentage would decrease as the number of covariates in the model increased. With this in mind, a slightly different modelling strategy was adopted when using this method. For the second model fitted, instead of containing all significant risk factors apart from self-assessed general health, as was the case for all other results presented so far, it was fitted including GHQ-12 score, age and sex only. This slightly different modelling strategy was employed here in

order to demonstrate more clearly the changes in percentage reduction as the number of covariates in the model changed.

A two-level Poisson model with log link was used to fit the continuous-time hazard models in MLwiN. A second-order polynomial was used to model the baseline hazard function.

Results from fitting the three models discussed above are presented in Table 8.7. Since the algebraic derivation of the Poisson model to be fitted to the aggregated dataset (Section 7.3.2.1) revealed that this model was the same as the original Poisson model (Section 5.3.3.1), this method was only deemed reliable if results obtained from these models were identical to those obtained from the original continuous-time hazard models (Table 5.3). Recall that, as there were slight differences in the models fitted in this section, results in Table 8.7 may only be compared to models B1 and B3 in Table 5.3. Comparing model E1 with model B1 and model E3 with B3 revealed identical results. As the parameter estimates are identical, no further discussion of results will be included in this section. For a full discussion refer back to Section 5.4.2.

The primary focus of this section was to demonstrate that grouping according to covariates could lead to a reduction in the size of the original expanded person-period dataset. Therefore, the percentage reduction in the expanded person-period dataset for each of the three models was of particular interest. The size of the original continuous-time person period dataset (Table 5.2) was just below 1.9 million. Table 8.8 displays the percentage reduction in the expanded dataset, for each of the three models E1, E2 and E3, compared to the original expanded dataset. This will be used to demonstrate how the percentage reduction in the original expanded dataset decreased as the number of covariates to be grouped on increased.

Table 8.7 - Results from ML continuous-time models grouped according to GHQ-12 score

	Model E1 Estimate(s.e)	Model E2 Estimate(s.e)	Model E3 Estimate(s.e)
Fixed			
Intercept (β_0)	-10.173(0.165)	-9.766(0.271)	-10.866(0.333)
Log(t_{ij}) (α_1)	0.227(0.117)	0.232(0.117)	0.203(0.116)
Log(t_{ij}) ² (α_2)	0.089(0.061)	0.091(0.061)	0.076(0.061)
GHQ-12 Score			
0	0.000	0.000**	0.000
1-2 (β_1)	0.699(0.226)	0.692(0.227)	0.483(0.229)
3-4 (β_2)	0.964(0.278)	0.987(0.279)	0.535(0.286)
5-12 (β_3)	1.353(0.218)	1.396(0.219)	0.713(0.236)
Sex			
Male		0.000	0.000
Female (β_4)		-0.197(0.173)	-0.107(0.187)
Age			
16-24		0.000	0.000
25-34 (β_5)		-0.403(0.284)	-0.245(0.287)
35-44 (β_6)		-0.186(0.275)	0.048(0.279)
45-54 (β_7)		-0.788(0.330)	-0.687(0.335)
55-64 (β_8)		-0.298(0.294)	-0.302(0.308)
65-74 (β_9)		-0.103(0.372)	0.207(0.386)
Marital Status			
Married/cohabiting			0.000
Other (β_{10})			0.391(0.181)
Receipts of Benefits			
No			0.000
Yes (β_{11})			0.605(0.210)
Smoking Status			
Non-Smoker			0.000
Current Smoker (β_{12})			0.722(0.215)
Ex-Smoker (β_{13})			0.016(0.301)
Employment Status			
Full-Time			0.000
Unemployed (β_{14})			0.541(0.267)
Part-Time (β_{15})			-0.317(0.254)
Self-Assessed Health			
Very Good			0.000
Good (β_{16})			0.505(0.225)
Fair (β_{17})			0.962(0.249)
Bad (β_{18})			0.191(0.553)
Very Bad (β_{19})			1.917(0.456)
Random			
Area Variation(σ_u^2)	0.255(0.263)	0.267(0.264)	0.246(0.246)

* $p_{\text{trend}} < 0.05$ ** $p_{\text{trend}} < 0.001$ **Table 8.8 - Percentage reduction when grouping covariates for continuous-time models**

Covariate Grouping	Size of New Dataset	% Reduction
GHQ-12 (model E1)	298 172	84%
GHQ-12, Age & Sex (model E2)	1 248 126	33%
Fully Adjusted (model E3)	1 794 049	4%

Grouping on GHQ-12 score only led to a fairly successful percentage reduction in the original continuous-time person-period dataset (Table 5.2). However, the table clearly demonstrates that, as the number of covariates in the model increased, the percentage reduction in the dataset decreased.

8.2.2 Results from Grouping According to Covariates in Discrete Time

In Section 8.1, it was shown that the greatest reduction in the discrete-time person-period dataset was achieved when the lengths of the intervals were defined according to when admissions occurred. Consequently, when fitting discrete-time hazard models to the grouped dataset, this was the approach taken. Table 8.3 detailed the discrete-time interval construction for this. The discrete-time aggregated dataset, with time intervals of varying length, was derived from that shown in Table 8.4. Table 8.9 below shows the aggregated discrete-time person-period dataset when data were grouped according to GHQ-12 score. The data are presented for the first postcode sector only.

Table 8.9 - Expanded dataset when grouping according to GHQ-12 score in discrete-time

Postcode	Cell	GHQ-12	Risk Set	No. at	No. of	No. of Total	Survival
Sector	ID	Score	Indicator	Risk in	Failures	Individual	Time
				Cell	in Cell	Failures	(days)
95001	1	0	1	10	0	26	0-400
95001	1	0	2	10	0	73	401-1620
95001	1	0	3	10	0	21	1621-2063
95001	1	0	4	10	0	17	2064-3046
95001	2	1 – 2	1	7	0	26	0-400
.
95001	2	1 – 2	4	7	0	17	2064-3046
95001	3	3 – 4	1	1	0	26	0-400
.
95001	3	3 – 4	4	1	0	17	2064-3046
95001	4	5 – 12	1	3	0	26	0-400
.
95001	4	5 - 12	4	3	0	17	2064-3046

Size of dataset = 8741

The columns in Table 8.9 above are exactly the same as those in the aggregated continuous-time person-period dataset in Table 8.6, and therefore all the interpretation is the same. The only exception is the ‘survival time’ column. In the continuous-time case this column referred to the number of days from interview at which an admission occurred; however, for the discrete-time case, this column now refers to a range of days constructed around the occurrence of admissions. Censoring may also occur within the intervals. Aggregating individuals within the same postcode sector according to GHQ-12 score reduced the size of the dataset to just below 9000 observations (cells) within postcode sectors. This provided a reduction of 84% from the original (ungrouped) discrete-time dataset with varied intervals (Table 8.4), which consisted of 54580 observations within postcode sectors. This also provided a reduction of over 99% on the original continuous-time expanded dataset (Table 5.2), containing just fewer than 1.9 million observations within postcode sectors.

As with the continuous-time hazard models, when aggregating the data in this way, interest was in investigating how the percentage reduction in the person-

period dataset changed as the number of covariates in the model changed. In order for this method to be reliable, results had to be the same or similar to those obtained before aggregation. Results from fitting the discrete-models to the aggregated data are shown in Table 8.10 below. The modelling strategy here was the same as for the continuous-time hazard models using the grouped data, and results were therefore comparable with models D1 and D3 in Table 8.5. The percentage reduction in the person-period dataset when using this method is displayed in Table 8.11.

When discrete-time hazard models were fitted in Section 8.1, the actual binary responses followed a Bernoulli distribution. However, when data were grouped according to postcode sector and covariates, the algebraic derivation (Section 7.3.3.1) revealed that the response was binomially distributed with denominator n_{gij} . Here, n_{gij} referred to the total number of individuals in a particular postcode sector with the same values for the covariates, i.e. the total number of individuals within each level-1 ‘cell’. As cell sizes will vary, weights should be used accordingly; however, as MLwiN assigns equal weights, a Poisson model was fitted instead, with the logarithm of the cell size used as the offset. Blocking factors were used to model the baseline hazard function. As with the continuous-time models above, a new aggregated dataset had to be created for each of the three models.

Comparing model F1 with D1 and F3 with D3 revealed similar parameter estimates for the fixed effects. Estimates of the random effects differed slightly when comparing model F1 to D1 and F3 to D3 with random effects being slightly underestimated using the aggregated data. These differences could be attributed to the fact that the Poisson model was being used instead of a Binomial model to model data that were grouped in discrete-time. This was because Binomial models fitted in MLwiN could not assign weights to account for the differences in cell sizes. As the directions of the regression parameter estimates were the same for models F1 and D1 and F3 and D3, a discussion of the conclusions can be found in Section 8.1.2.

Table 8.10- Results from ML discrete-time models grouped according to GHQ-12 score

	Model F1 Estimate(s.e)	Model F2 Estimate(s.e)	Model F3 Estimate(s.e)
Fixed			
Intercept (β_0)	-6.927(0.231)	-6.514(0.316)	-7.228(0.325)
t2 _{ij} (α_1)	1.045(0.228)	1.045(0.228)	1.061(0.228)
t3 _{ij} (α_2)	-0.167(0.293)	-0.165(0.293)	-0.131(0.294)
t4 _{ij} (α_3)	0.082(0.312)	0.090(0.313)	0.023(0.313)
GHQ-12 Score			
0	0.000	0.000	0.000
1-2 (β_1)	0.697(0.226)	0.689(0.227)	0.481(0.229)
3-4 (β_2)	0.960(0.278)	0.977(0.279)	0.523(0.286)
5-12 (β_3)	1.342(0.218)	1.384(0.219)	0.692(0.236)
Sex			
Male		0.000	0.000
Female (β_4)		-0.188(0.173)	-0.095(0.187)
Age			
16-24		0.000	0.000
25-34 (β_5)		-0.401(0.283)	-0.246(0.287)
35-44 (β_6)		-0.187(0.275)	0.040(0.279)
45-54 (β_7)		-0.795(0.330)	-0.703(0.335)
55-64 (β_8)		-0.317(0.294)	-0.336(0.308)
65-74 (β_9)		-0.190(0.372)	0.090(0.386)
Marital Status			
Married/cohabiting			0.000
Other (β_{10})			0.403(0.181)
Receipts of Benefits			
No			0.000
Yes (β_{11})			0.588(0.209)
Smoking Status			
Non-Smoker			0.000
Current Smoker (β_{12})			0.702(0.215)
Ex-Smoker (β_{13})			0.010(0.301)
Employment Status			
Full-Time			0.000
Unemployed (β_{14})			0.552(0.267)
Part-Time (β_{15})			-0.308(0.254)
Self-Assessed Health			
Very Good			0.000
Good (β_{16})			0.524(0.225)
Fair (β_{17})			0.981(0.250)
Bad (β_{18})			0.236(0.552)
Very Bad (β_{19})			1.944(0.455)
Random			
Area Variation(σ_u^2)	0.263(0.264)	0.274(0.264)	0.215(0.245)

The percentage reduction in the person-period dataset after aggregation is shown in Table 8.11 for each of the three models. Recall that the size of the original continuous-time person-period dataset (Table 5.2) comprised just fewer than 1.9 million observations within postcode sectors. The ungrouped discrete-time dataset when using varied intervals (Table 8.4) comprised just fewer than 55000 observations within postcode sectors. Table 8.11 displays the percentage reduction when comparing the aggregated dataset to each of these.

Table 8.11 - Percentage reduction when grouping covariates for discrete-time models with varying intervals

Covariate Grouping	Size of New Dataset	% Reduction on Original Continuous Data	% Reduction on Discrete Data (varied intervals)
GHQ-12 (model F1)	8741	99.5%	84%
GHQ-12, Age & Sex (model F2)	36 451	98%	33%
Fully Adjusted (model F3)	52 371	97%	4%

Fitting discrete-time hazard models to the aggregated dataset led to a substantial reduction in the original continuous-time dataset for all three models. However, when comparing the size of the discrete-time aggregated dataset to the ungrouped one, only grouping on GHQ-12 score led to a considerable percentage reduction in the dataset. Again, this demonstrates that the percentage reduction in the dataset decreased as the number of covariates in the model increased.

8.2.3 Summary: Grouping According to Covariates

Based on the assumption that all individuals within the same postcode sector with the same values for covariates included in a particular model are at risk at the same time, this section fitted multilevel survival models using aggregated datasets as a means of reducing the size of the original person-period dataset in Table 5.2. Multilevel continuous-time and discrete-time hazard models were fitted to aggregated datasets and the percentage reduction in the ungrouped continuous-time person-period dataset (and the ungrouped person-period

discrete-time dataset) was assessed. As well as observing the percentage reduction in the original expanded dataset for the models, it was also important to monitor the parameter estimates. For the grouping covariates method to be reliable, it was important for parameter estimates to be identical (or at least similar in the discrete-time case) to those obtained using the original ungrouped datasets.

Fitting continuous-time hazard models to the aggregated dataset (Table 8.7) produced identical parameter estimates to those obtained with the original continuous-time dataset (Table 5.3). However, Table 8.8 revealed that the size of the dataset was only reduced considerably when the data were grouped according to GHQ-12 score alone. This was also the case when fitting discrete-time hazard models. Although fitting discrete-time models led to a vast reduction in the continuous-time person-period dataset, it can be observed that, when comparing the aggregated discrete-time dataset to the ungrouped discrete-time dataset, the reduction was only considerable when grouping on GHQ-12 score.

To summarise, the grouping covariates method can be successful in reducing the size of the original expanded dataset when the number of covariates to be grouped on is small and, in particular, when time is treated as a discrete variable. However, as the number of covariates in the model, and therefore the number of covariates to be grouped on increases, the percentage reduction in the expanded person-period dataset decreases considerably. Recall also that the number of individuals within each higher-level unit can affect the percentage reduction in the ungrouped person-period dataset. In the SHeS dataset there were approximately 25 individuals per postcode-sector on average. Because this number is fairly small, there may be fewer individuals within each postcode-sector sharing the exact same values for the covariates to be grouped on. This is especially true when grouping according to all covariates in the fully adjusted model. This explains why the method did not perform well for the models including a larger number of covariates when applied to the SHeS dataset.

A possible disadvantage of using the grouping covariates method is the process of having to create a new grouped dataset to generate the new level-1 'cell' combinations as the covariates included in the model change. This suggests that

this method should not be used during model selection, but only once a final modelling strategy has been selected. Model selection could be carried out by fitting survival models to the ungrouped datasets; however, this does not eliminate the problems associated with fitting multilevel survival models to very large datasets, which is the intended purpose of the grouping covariates method. Therefore, it may be worthwhile to use multilevel logistic regression models during the model selection process, and then proceed to use the grouping covariates method once all final models have been selected.

8.3 Bayesian Survival Models

8.3.1 Proportional Hazards Models using a Bayesian Approach

All results presented in Chapter 5 and Sections 8.1 and 8.2 were obtained from fitting proportional hazards (PH) models in MLwiN, using first-order PQL as the method of estimation. This section adopts a Bayesian approach to fitting proportional hazards models. Since fitting proportional hazards models in WinBUGS still requires the appropriate data expansion such that each subject has a line of data corresponding to each risk set they survived, it may not seem worthwhile fitting these models again in WinBUGS; however, results obtained here were compared to those obtained in MLwiN in order to check that MCMC estimation was producing similar results to PQL estimation. Confirmation of this then permitted the fitting of frailty models in WinBUGS.

In order to ensure a fair comparison between the two methods of estimation (MCMC and PQL), the proportional hazards model fitted using a Bayesian approach was exactly the same as that fitted using a frequentist approach in Section 5.4. To reiterate, a continuous-time Poisson model with log link using a second-order polynomial to smooth the blocking factors was fitted in WinBUGS. Since time was treated as continuous, the response was the length of time in days from Scottish Health Survey interview until first psychiatric admission. As usual, observations were censored if the subject died or did not experience a psychiatric admission during follow-up. The data expansion was also the same as

that in Chapter 5, and therefore the expanded person-period dataset consisted of just fewer than 1.9 million observations within individuals.

As the purpose of fitting the proportional hazards models using a Bayesian approach was just to confirm that MCMC estimation was obtaining the same results as PQL estimation, only the model including just GHQ-12 score was fitted here. Results from this model are presented in Section 8.3.1.1.

8.3.1.1 Results from fitting Proportional Hazards Models in WinBUGS

When employing a Bayesian approach to fit the PH models in this section, the postcode sector residuals were given a Normal prior with mean zero and precision $1/\sigma_u^2$. As discussed in Section 7.4.4.2, the higher-level standard deviation was given a vague uniform(0,3) prior. A value of 3 was chosen for the upper bound on the standard deviation (i.e. 9 on the variance) so that it was large enough that it would not be reached. It was known from previous results that the variance had been considerably smaller than 9. As no prior information was available on the parameters of the fixed effects, they were assigned vague Normal priors with zero mean and precision 0.0001. Results are presented in Table 8.12.

Initial values were chosen based on the parameter estimates obtained from fitting the continuous-time proportional hazards models in MLwiN (Table 5.3). Because it was predicted that the models would take a while to run due to the vast size of the expanded dataset, only 1 chain was run using the full dataset. Prior to this, some exploratory analyses were performed on a subset of the full expanded dataset based on the first 25 postcode sectors. This gave an idea of the size of the burn-in required for stationarity, as well as the number of iterations required after convergence for monitoring parameter estimates. A burn-in of 10000 iterations appeared to adequately achieve convergence with a further 10000 updates after convergence.

All parameter estimates obtained in Table 8.12 below should be compared to the parameter estimates in model B1, presented in Table 5.3. As usual, results

presented below are for subjects with no psychiatric admissions prior to survey interview. Recall that MCMC estimation was used to obtain parameter estimates.

Table 8.12 - Results from PH Models using a Bayesian Approach

	Estimate	95% Credible Interval
Fixed		
Intercept (β_0)	-10.32	(-10.72, -9.95)
Log(t_{ij}) (α_1)	0.223	(-0.005, 0.461)
Log(t_{ij}) ² (α_2)	0.081	(-0.048, 0.201)
GHQ-12 Score		
0 (β_1)	0.000	
1-2 (β_2)	0.698	(0.254, 1.15)
3-4 (β_3)	0.949	(0.388, 1.488)
5-12 (β_4)	1.351	(0.926, 1.782)
Random		
Area Variation (σ_u^2)	0.288	(0.011, 0.779)

CPU time for the model displayed in Table 8.12, as recorded by WinBUGS, was 355 558 seconds. In reality, however, the time until completion was approximately 9 days.

Since the purpose of running this model was just to compare parameter estimates using MCMC and PQL methods of estimation, no convergence diagnostics, such as trace plots, will be included here. Instead, parameter estimates from Table 8.12 should just be compared to those obtained from fitting the Poisson model in MLwiN as displayed in Table 5.3.

The parameter estimates obtained for the fixed effects from the PH model using a Bayesian approach were very similar to those obtained from the same models using a frequentist approach in MLwiN. The postcode sector variance was slightly different using the Bayesian approach, and the 95% credible interval (CrI) was very wide. This may indicate that a bigger burn-in period was required.

8.3.1.2 Summary of Bayesian Proportional Hazards Model Results

Section 8.3.1 discussed the application of Bayesian methods to survival modelling, and why these methods may be more attractive than taking a frequentist approach. Subsequent sections in this chapter will proceed to fit frailty models using a Bayesian approach; however, it was firstly necessary to demonstrate that MCMC estimation would produce similar estimates to those obtained using PQL estimation. This ensures that Bayesian methods for fitting multilevel survival models in WinBUGS are comparable to frequentist methods employed to fit these models in MLwiN.

Comparison of MCMC and PQL estimation was carried out by fitting the same continuous-time proportional hazards model using a Bayesian approach in WinBUGS as was fitted previously in MLwiN (Section 5.4). The PH model took a considerably longer time to run in WinBUGS using MCMC estimation than in MLwiN using PQL estimation; however, as parameter estimates using the two approaches (Bayesian and frequentist) were similar, this ensured that estimates obtained using these different methods of estimation were comparable. Confirmation of this now means that a new type of model may be tested as an alternative to fitting continuous-time proportional hazard models in MLwiN - the frailty model using a Bayesian approach. Results from these models are presented in Section 8.3.2.

8.3.2 Fitting Frailty Models in WinBUGS

This section will present results obtained from fitting the shared frailty model in WinBUGS. As discussed in Section 7.4.4.1, a Weibull distribution is assumed for the survivor function with shape parameter, r , and scale parameter, μ_{ij} . While the Poisson model fitted in MLwiN required the dataset to be expanded into a person-period dataset, thus leading to a vast increase in the size of the dataset, no such expansion is required to fit frailty models in WinBUGS.

Since Section 8.3.1 of this chapter confirmed that PQL and MCMC estimation were obtaining similar parameter estimates, results from the shared frailty

model can be compared with results from the original Poisson model in Table 5.3. The Poisson model produced estimates of hazard ratios; therefore, in order to be able to compare parameter estimates from the Poisson model and the Weibull model fitted in WinBUGS, it was important to check that the parameter estimates from the Weibull model fitted in WinBUGS could also be interpreted as hazard ratios. Recall from 7.4.4 that the hazard function from fitting the additive frailty model in WinBUGS is given as

$$h(t_{ij} | x_{ij}, u_j) = \mu_{ij} r t_{ij}^{r-1},$$

where

$$\log(\mu_{ij}) = \alpha + \beta^T x_{ij} + u_j.$$

Consider the baseline hazard for which all values of the covariates are zero, and therefore the model contains an intercept, α , (and possibly random effects) only. Consider also the hazard of event for an individual with covariate vector x . Then, in the proportional hazards model, $\exp(\beta^T x)$ represents the hazard ratio, i.e. the hazard of event at time t for an individual with covariate vector x relative to the baseline hazard. If the ratio of these hazards equals $\exp(\beta^T x)$, then the regression parameters from the additive frailty model fitted in WinBUGS may be interpreted as hazard ratios.

$$\begin{aligned} \frac{h(t_{ij} | x_{ij}, u_j)}{h(t_0 | u_j)} &= \frac{[\exp(\alpha + \beta^T x_{ij} + u_j)] r t_{ij}^{r-1}}{[\exp(\alpha + u_j)] r t_0^{r-1}} \\ &= \exp(\beta^T x_{ij}) . \end{aligned}$$

Therefore, the regression parameter estimates obtained from fitting the additive frailty model in WinBUGS may be interpreted as hazard ratios.

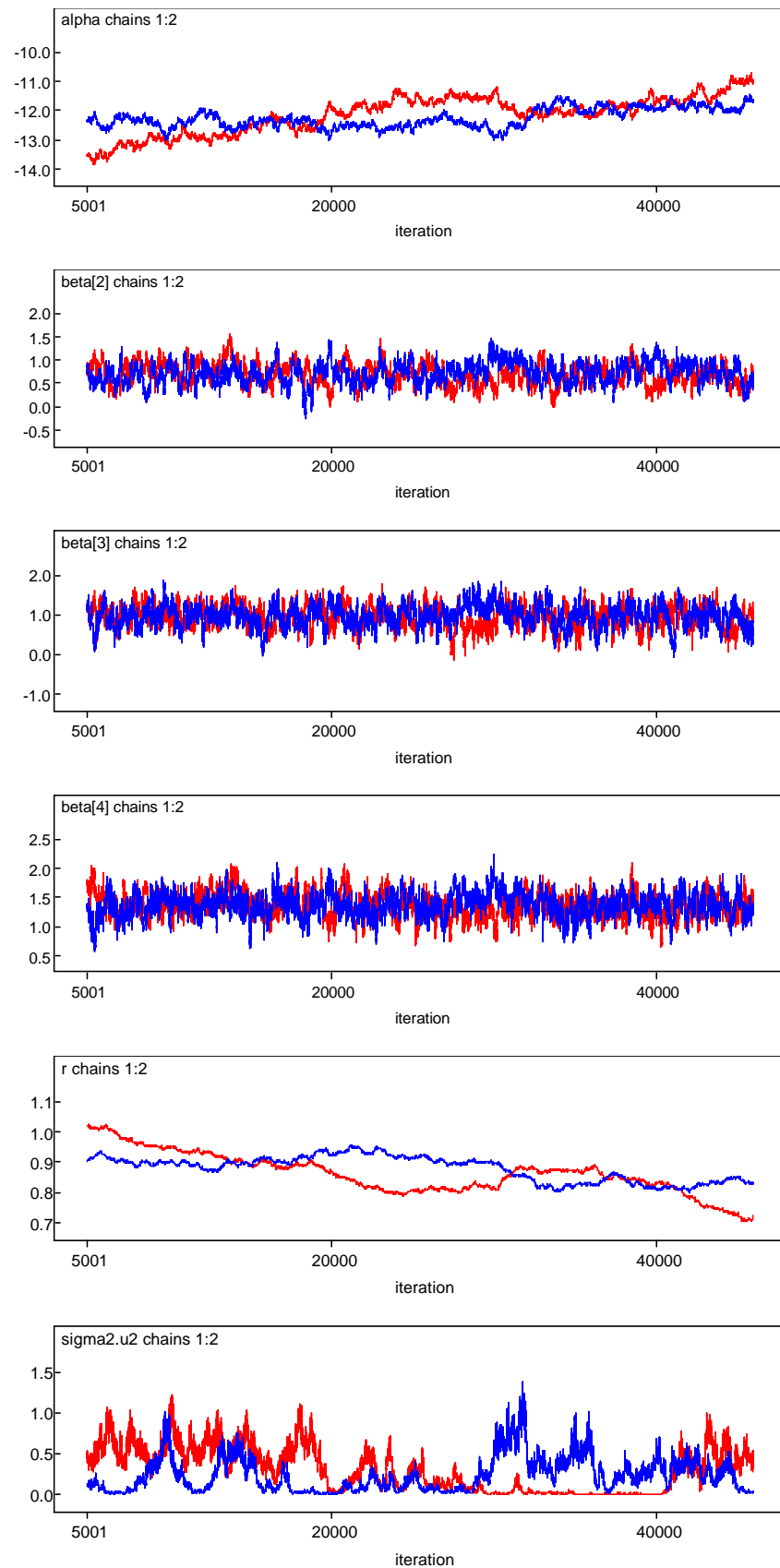
8.3.2.1 Results from Bayesian Frailty Models

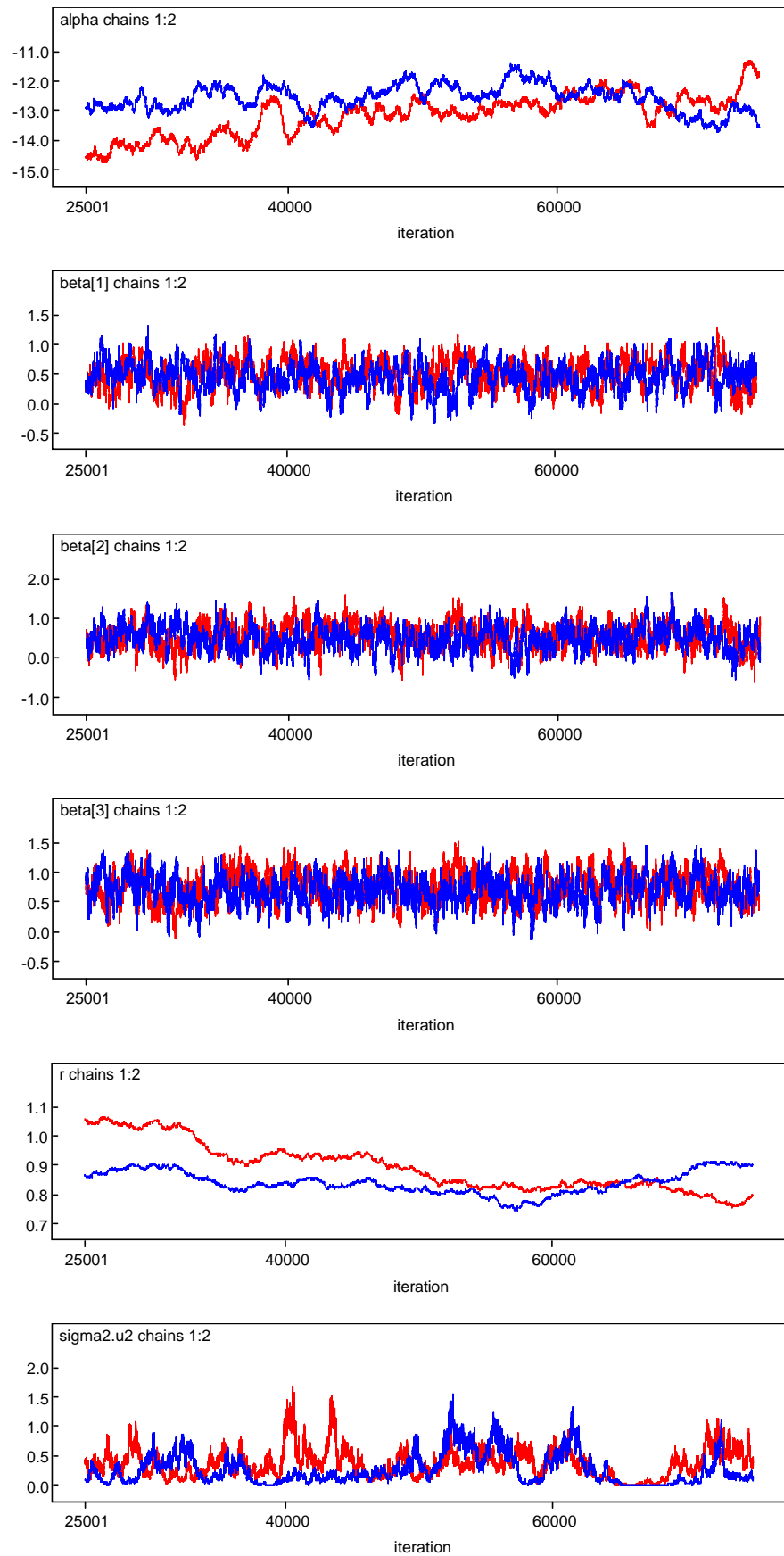
This section presents results obtained from fitting a Weibull model to the Scottish Health Survey data in WinBUGS. As before, the response was time until first psychiatric admission as measured in days from Scottish Health Survey interview, with any individuals who did not experience the event or who died during follow-up being censored. Recall also that the primary interest was to investigate the effect of GHQ-12 score on the hazard of first psychiatric admission. Information was also available on a range of demographic, socioeconomic and lifestyle risk factors.

Table 8.13 below displays results from fitting two Weibull models - one containing GHQ-12 score only, and the other containing GHQ-12 score plus other risk factors which were found to be significant when fitting the continuous-time model in Section 5.4, referred to here as the ‘full model’. In other words, results from Table 8.13 below should be compared to models B1 and B3 in Table 5.3. Recall from Section 7.4.4.2 that the random effects (frailties) were given a log-Normal prior, thus making the model a log-Normal frailty model. The random effects standard deviation was given a Uniform prior, the shape parameter a log-Normal prior, and finally, regression coefficients were given Normal priors. Initial values were chosen based on parameter estimates obtained from fitting the continuous-time Poisson model. For the model containing GHQ-12 score only, a burn-in of 5000 iterations seemed to adequately achieve convergence, with a further 41000 iterations after convergence to obtain posterior estimates. In the model containing GHQ-12 score and all other significant risk factors, 25000 iterations were required for burn-in, with a further 50000 iterations on attaining convergence. Convergence was assessed using trace plots (Figures 8.1 and 8.2) and Gelman-Rubin plots (Figures 8.3 and 8.4). Note that, for the model containing all significant covariates i.e. the full model, Figures 8.2 and 8.4 only display trace plots and Gelman-Rubin plots for the intercept, GHQ-12 regression parameters, shape and random effects variance. Trace plots and Gelman-Rubin plots for all other significant covariates can be found in Appendix 3.

Table 8.13 - Results from Weibull model

	GHQ-12 Only		Full Model	
	Estimate	Credible Interval	Estimate	Credible Interval
Fixed				
Intercept (α)	-12.2	(-13.26, -11.27)	-12.87	(-14.36, -11.78)
GHQ-12 Score				
0	0.000		0.000	
1-2 (β_1)	0.706	(0.27, 1.14)	0.475	(0.001, 0.92)
3-4 (β_2)	0.956	(0.37, 1.48)	0.511	(-0.10, 1.09)
5-12 (β_3)	1.368	(0.97, 1.78)	0.725	(0.26, 1.18)
Sex				
Male			0.000	
Female (β_4)			-0.123	(-0.50, 0.25)
Age				
16-24			0.000	
25-34 (β_5)			-0.285	(-0.82, 0.29)
35-44 (β_6)			0.024	(-0.51, 0.58)
45-54 (β_7)			-0.717	(-1.46, -0.02)
55-64 (β_8)			-0.321	(-0.97, 0.28)
65-74 (β_9)			0.269	(-0.46, 0.99)
Marital Status				
Married/cohabiting			0.000	
Other (β_{10})			0.351	(-0.01, 0.72)
Receipts of Benefits				
No			0.000	
Yes (β_{11})			0.639	(0.22, 1.05)
Smoking Status				
Non-Smoker			0.000	
Current Smoker (β_{12})			0.728	(0.32, 1.21)
Ex-Smoker (β_{13})			-0.032	(-0.69, 0.60)
Employment Status				
Full-Time			0.000	
Unemployed (β_{14})			0.504	(-0.05, 1.04)
Part-Time (β_{15})			-0.339	(-0.82, 0.14)
Self-Assessed Health				
Very Good			0.000	
Good (β_{16})			0.446	(-0.002, 0.90)
Fair (β_{17})			0.897	(0.43, 1.38)
Bad (β_{18})			0.001	(-1.24, 1.03)
Very Bad (β_{19})			1.783	(0.81, 2.67)
Shape (r)	0.870	(0.74, 0.98)	0.866	(0.76, 1.04)
Random				
Area Variation(σ_u^2)	0.263	(0.001, 0.807)	0.307	(0.001, 0.91)

**Figure 8.1 - Trace plots for GHQ-12 only model**

**Figure 8.2 - Trace plots for full model**

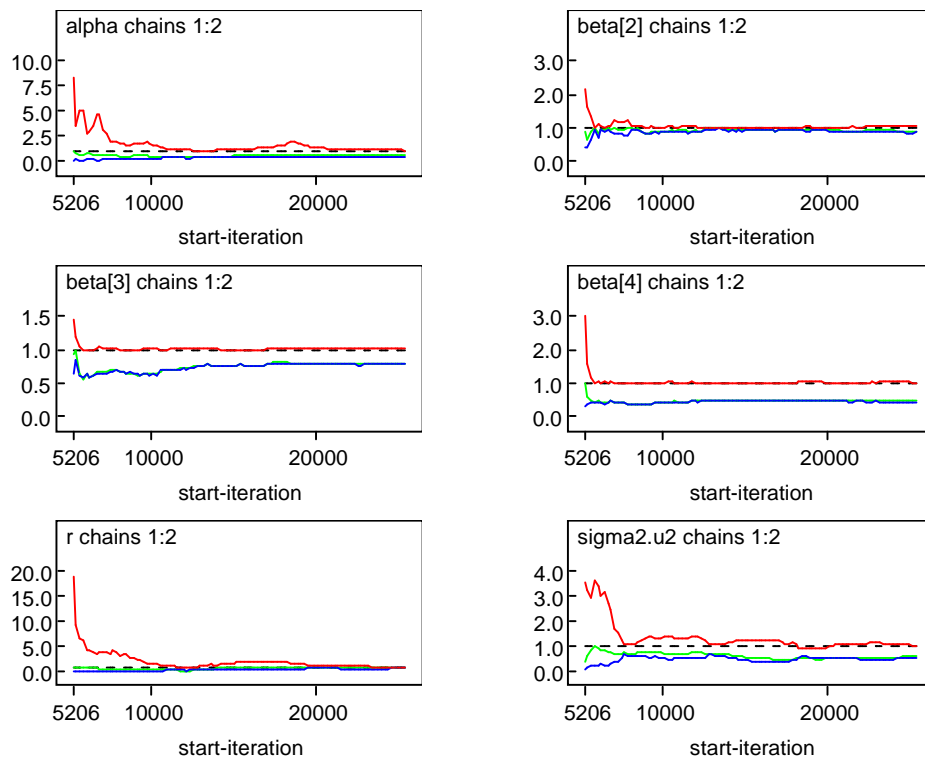


Figure 8.3 - Gelman-Rubin plots for GHQ-12 only model

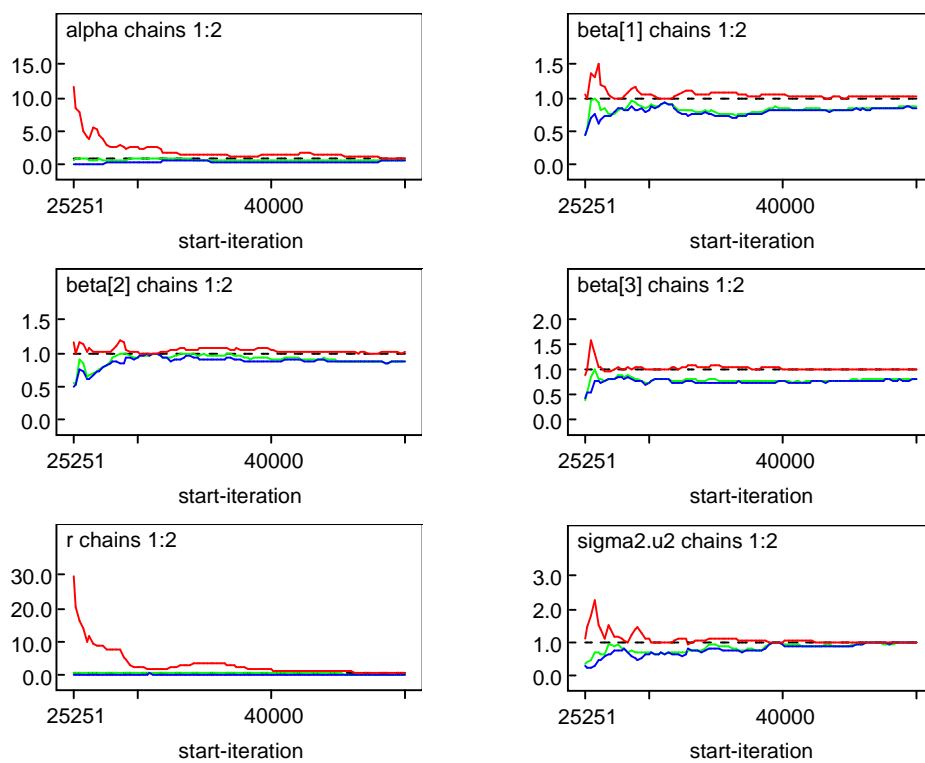


Figure 8.4 - Gelman Rubin Plots for full model

Table 8.14 - MC Error as a percentage of posterior standard deviation

Parameters	GHQ-12 Only Model			Full Model		
	MC Error	SD	MCE as % of SD	MC Error	SD	MCE as % of SD
α	0.02531	0.5125	4.9%	0.03077	0.6542	4.7%
β_1	0.00957	0.2291	4.2%	0.00927	0.2333	4.0%
β_2	0.01111	0.2828	3.9%	0.01142	0.3068	3.7%
β_3	0.00782	0.2064	3.8%	0.00886	0.2405	3.7%
r	0.00281	0.0566	5.0%	0.00329	0.0695	4.7%
σ_u^2	0.01167	0.2417	4.8%	0.01132	0.2489	4.5%

Table 8.13 displays parameter estimates and 95% credible intervals obtained from fitting an additive log-Normal frailty model in WinBUGS, where a Weibull distribution was assumed for the survival times. CPU time was 17390 seconds and 64047 seconds for the GHQ-12 only model and full model respectively.

On comparing parameter estimates from the GHQ-12 and full models to models B1 and B3 in Table 5.3 respectively, parameter estimates generally appeared to be fairly similar for both models, and the direction of the parameter estimates from using the two different modelling approaches, i.e. the Poisson model and the additive frailty model, were the same. However, there were some points to note from the results produced from fitting the additive frailty model. In both the GHQ-12 only model and the full model, for most of the regression parameters and the higher-level variance, σ_u^2 , the 95% credible intervals were quite wide. This may suggest that the burn-in period was not long enough to successfully achieve convergence; hence, more simulations may have been required to improve inference about the target distribution. Examination of the trace plots in Figure 8.1 showed that the chains in the trace plots for each of the regression parameters from the GHQ-12 model were not mixing perfectly, and might have benefited from a bigger burn-in. However, the Gelman-Rubin plots in Figure 8.3 for the same parameters suggested that convergence had been successfully attained after 5000 iterations. Also, from Figure 8.1, it was clear that the simulations for the intercept, α , and for the shape parameter, r , had not stabilised as the chains in these plots were not mixing well or stabilising around a sample value. The chains for these two parameters also appeared to be

correlated with each other. Finally, from Figure 8.1 it was observed that the Gibbs sampler for the random effects variance was getting stuck near zero. Once trapped here, the simulation may take a long time to escape [258]. A parameter expansion scheme may be adopted to overcome slow convergence. This will be considered in Section 8.3.5. Similar patterns for the full model were observed in Figures 8.2 and 8.4.

Another way of assessing the accuracy of the posterior estimates is by comparing the Monte Carlo error (MC error) and the sample standard deviation, as was discussed in Section 7.4.6.3. A rule of thumb is that the MC error should be less than around 5% of the sample standard deviation. For the GHQ-12 only model, Table 8.14 shows that this was the case for all parameters. However, for most parameters, the MC error was only just less than 5% of the sample standard deviation, suggesting that more iterations may have been required after achieving convergence. The same was true of the full model.

The shape parameter in the GHQ-12 only model in Table 8.13 was less than 1 (= 0.870) with 95% credible interval wholly less than 1. This suggested that the hazard rate of event, when adjusting for GHQ-12 score, was strictly decreasing in a nonlinear pattern as time increases. When the model was adjusted for all further significant covariates, the shape parameter was still less than 1 (= 0.866); however, the 95% credible interval overlapped 1, indicating that it was plausible that the hazard rate remained constant as time increased.

Several areas for consideration arose from fitting the additive frailty model to the SHeS dataset. Firstly, the chains for the shape parameter and intercept displayed in the trace plots in Figures 8.1 and 8.2 were very highly correlated. Secondly, the Gibbs sampler was prone to getting trapped near zero for the higher-level variance. As few individuals experienced the event of interest, there were a large number of censored observations (approximately 99%). One notion was that the problems were a consequence of the high percentage of censoring, with the Weibull model perhaps not providing a 'good fit' in the presence of many censored observations. To investigate this further a simulation study was carried out. Full details are given in Section 8.3.3.

8.3.3 Fitting Bayesian Frailty Models to a Simulated Dataset

In the previous section it was discussed that the high percentage of censoring in the SHeS dataset could be problematic when trying to fit the Weibull model. To investigate this notion, a simulation study was carried out by simulating two datasets - one which contained no censored observations and another which contained a percentage of censored observations similar to that of the SHeS dataset. Fitting models to both of these simulated datasets and comparing results would indicate whether or not the high percentage of censoring was posing a difficulty when trying to fit the Weibull model.

The simulated datasets had to be similar to the SHeS dataset in terms of size. Recall that in the SHeS dataset there were 15305 individuals (with no psychiatric admission prior to survey interview) nested within 624 postcode sectors; therefore, the simulated datasets were specified to contain 15000 level-1 units within 600 level-2 units. Recall also that the SHeS dataset was created from information obtained from two different survey years, namely 1995 and 1998. It is clear that those surveyed in 1995 would have a follow-up time of around 9 years, whereas those surveyed in 1998 would have a shorter-follow up time of 6 years (follow-up time was until 2004). The differences in follow-up times also had to be accounted for when generating the simulated datasets. Parameter estimates obtained from fitting the continuous-time Poisson model to the SHeS data (Table 5.3) were used calculate the scale parameter, μ . This was required when simulating the Weibull survival times, t , which were calculated using the distribution's inverse probability function [259] such that

$$t = \frac{\mu}{r} \times [-\ln(rnd)]^{\frac{1}{r}},$$

where 'rnd' corresponded to the random numbers generated from the Uniform distribution on the interval (0,1). The simulated datasets were created in MLwiN and were then transferred into WinBUGS to fit the Weibull model.

The first point to investigate was the correlation in the chains for the intercept, α , and the shape parameter, r . It was of interest to observe whether or not the percentage of censored observations would have an effect on how these

parameters behaved. Two models were fitted to both the simulated dataset with no censoring and the simulated dataset with a percentage of censoring similar to that of the actual SHeS dataset. The first model contained an intercept only (i.e. no covariates or random effects) and fixed the shape parameter at 0.9 in the Weibull distribution for survival times (recall from Table 8.13 that 0.9 was the parameter estimate obtained for the shape parameter, r , when fitting the Weibull model to the SHeS dataset); the second model was similar except that r was not fixed and was specified to follow a log-Normal distribution. Parameter estimates and 95% credible intervals are displayed in Table 8.15. Trace plots and Gelman-Rubin plots are displayed in Figures 8.5 and 8.6.

Table 8.15 - Comparing intercept-only models between all-event and highly censored simulated datasets

	r fixed at 0.9		r not fixed	
	Estimate	95% CrI	Estimate	95% CrI
No Censoring				
Intercept (α)	-10.0	(-10.02, -9.99)	-9.999	(-10.12, -9.88)
Shape (r)	-	-	0.900	(0.89, 0.91)
95% Censoring				
Intercept (α)	-10.06	(-10.13, -9.99)	-10.48	(-11.08, -10.13)
Shape (r)	-	-	0.953	(0.91, 1.03)

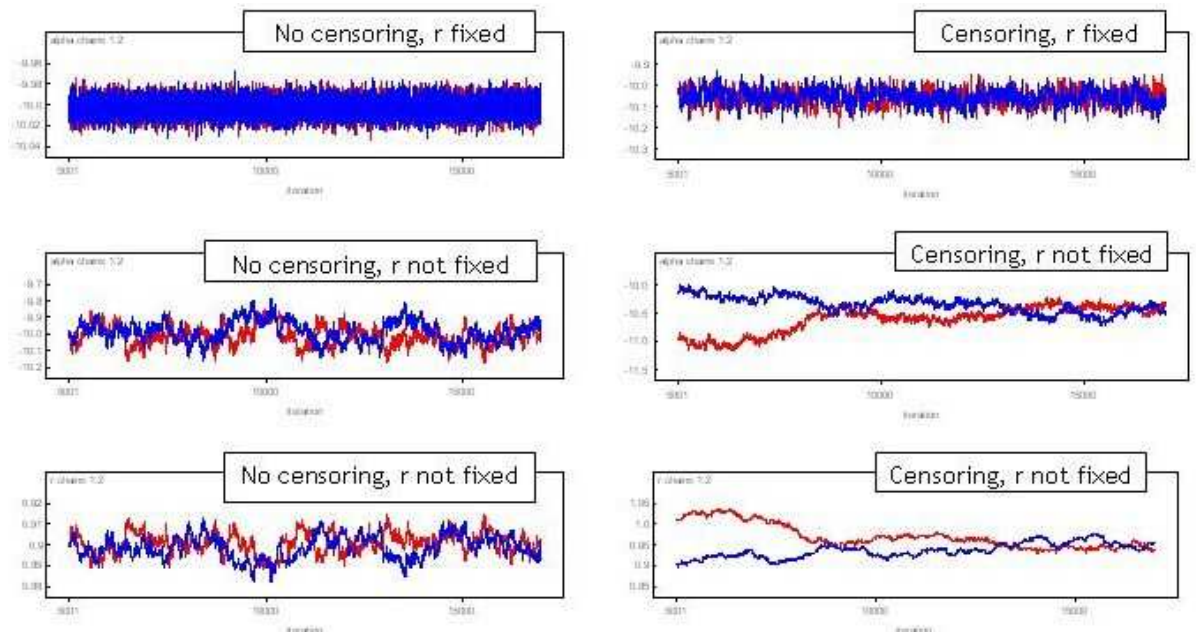


Figure 8.5 - Trace plots for intercept-only models from all-event & highly censored simulated datasets

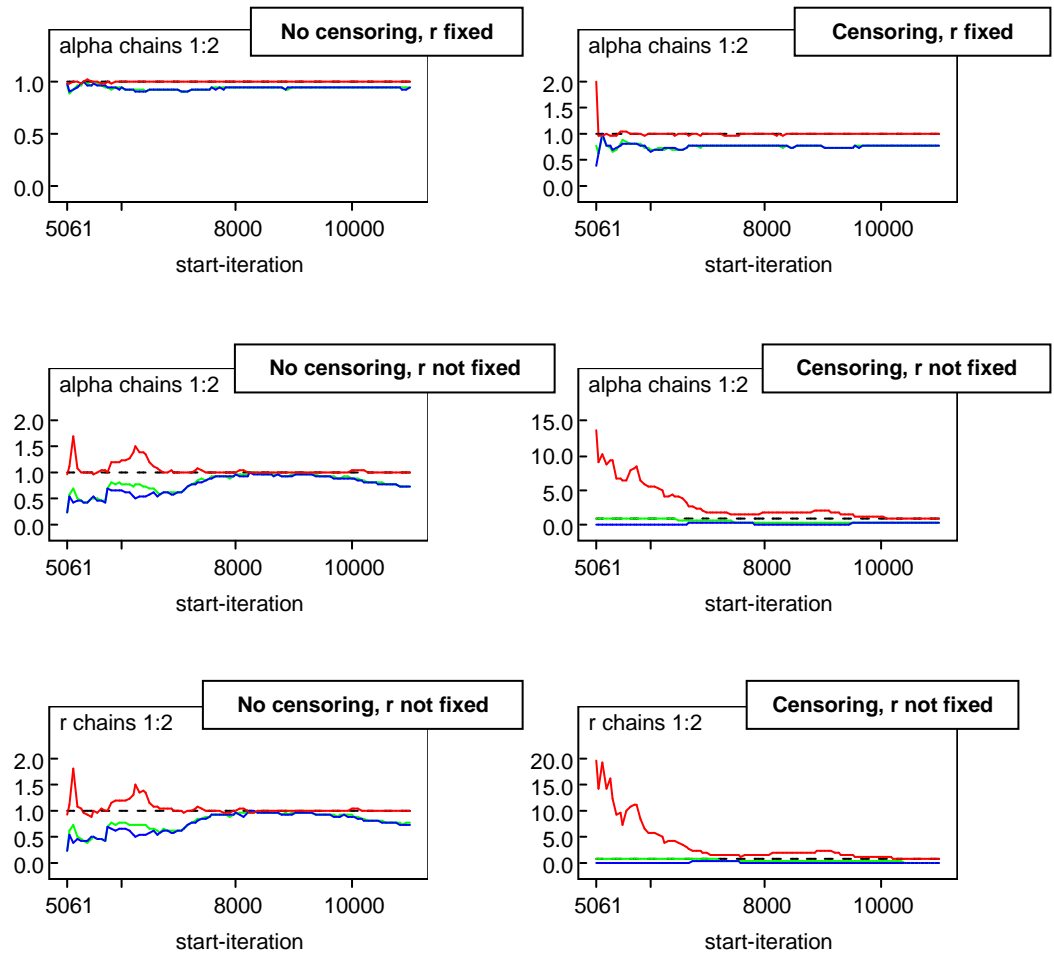


Figure 8.6 - Gelman-Rubin plots for intercept-only models from uncensored & highly censored simulated datasets

As in the frailty model fitted in Section 8.3.2.1, the intercept, α , was given a $\text{Normal}(0, 0.0001)$ prior, and the shape parameter, r , a $\text{log-Normal}(0, 0.1)$ prior. For each of the four models in Table 8.15 above, a burn-in period of 5000 iterations was used before running a further 12000 iterations to obtain the parameter estimates displayed. The average CPU time for the four models was 2644 seconds.

When comparing results from fitting the four models displayed in Table 8.15, generally there was not much of a difference in the parameter estimates for α and r respectively. However, there were some points to note. It was mentioned previously that parameter estimates obtained from fitting the Poisson model to the SHeS data (Table 5.3) were used in the simulation, i.e. a value of

-10 for alpha. The value of 0.9 for r was obtained from fitting the Weibull model to the SHeS data (Table 8.13). When examining the results in Table 8.15, the parameter estimates for alpha and r (where applicable) were all close to these respective values; however, when looking at results from the model containing both alpha and r which was fitted to the simulated dataset with a high percentage of censoring, the 95% credible interval for alpha did not include -10 and, similarly, the 95% credible interval for r did not include 0.9. The trace plots in Figure 8.5 were used to determine how well the parameters are behaving. For the model containing alpha only fitted to the simulated dataset with no censoring, the trace plot indicated that the multiple chains were mixing well, and hence convergence looked reasonable. The parameter estimate of alpha from this model was exactly -10, with a very narrow 95% CrI. When the same model (intercept only) was fitted to the simulated dataset containing the high percentage of censoring, the multiple chains in the trace plot were not mixing quite as well as when there were no censored observations; however, convergence still looked reasonable, and the Gelman-Rubin plot in Figure 8.6 also indicated that a burn-in period of 5000 seemed sufficient enough to achieve convergence. The 95% CrI, however, was slightly wider when censoring was present than when the same model was fitted to the simulated dataset containing no censoring.

When the shape parameter was no longer fixed at 0.9 in the Weibull distribution, the multiple chains in the trace plot for the model (now containing both alpha and r) fitted to the simulated dataset with no censoring were not mixing very well for either parameter, with evidence of correlation between the chains for the two parameters. The Gelman-Rubin plots in Figure 8.6 indicated that a bigger burn-in period may have been required (perhaps around 9000 iterations). When comparing the two models fitted to the simulated dataset containing no censored observations, the 95% credible interval for the intercept in the model when r was not fixed was wider than that obtained when r was fixed at 0.9; however, -10 was still included in the range of plausible values. Finally, the multiple chains in trace plots for the model fitted to the highly censored simulated dataset when r was not fixed at 0.9 were not mixing at all for either parameter and again there appeared to be correlation between the chains for the two parameters. Neither of the 95% credible intervals for alpha and r

overlapped the respective values of -10 or 0.9, which were the values expected for those parameters.

Up to this point, the simulation study showed that having a high percentage of censored observations had a slight effect on the results. Parameter estimates were the least precise when censoring was present, as opposed to when there were no censored observations; however, there was still correlation between the chains for the intercept and the shape parameter when there were no censored observations, although the multiple chains were mixing better. It is of interest to reduce the correlation in the Markov chains in order to reduce the number of iterations required, thus speeding up computing time. Ways of eliminating this correlation are considered in Section 8.3.4.

8.3.4 Reducing Correlation in the Weibull Model

Consider a Weibull distribution with shape parameter r and scale parameter μ . In WinBUGS notation this is $X \sim \text{dweib}(r, \mu)$ and the probability density function, $p(x)$, is given as

$$p(x) = r \mu x^{r-1} \exp(-\mu x^r); \quad x > 0.$$

The expectation of X is thus given as

$$E(X) = \mu^{-1/r} \Gamma(1 + 1/r).$$

The value of $E(X)$ will be pinned down by the data and

$$\mu^{-1/r} \Gamma(1 + 1/r) \approx \text{constant}, \quad k \text{ say}.$$

Taking the natural logarithm, this becomes

$$-1/r \log(\mu) + \log[\Gamma(1 + 1/r)] \approx k$$

$$\text{i.e.} \quad \log(\mu) \approx -r\{k - \log[\Gamma(1 + 1/r)]\}$$

Equation 8.1

Suppose, for the purpose of illustration, that the model to be fitted contains an intercept, α , only, i.e. there are no covariates or random effects. Then $\log(\mu) = \alpha$. Thus, from Equation 8.1, it is clear that the posterior negative correlation observed between α and r is not surprising (especially if r is close to 1).

Consider, instead, the probability density function for an alternative parameterisation of the Weibull distribution,

$$p(x) = r/\lambda(x/\lambda)^{r-1}\exp[-(x/\lambda)^r]; \quad x > 0, \\ = (r/\lambda^r)x^{r-1}\exp[-(x^r/\lambda^r)] ,$$

for a Weibull distribution with shape parameter r and scale parameter λ . Now the expected value of X is given as

$$E(X) = \lambda\Gamma(1 + 1/r) .$$

This re-parameterisation should lead to a posterior for (r, λ) with less correlation. It is clear from the re-parameterisation that

$$\mu = 1/\lambda^r .$$

Thus, for a model containing an intercept only the model is written in WinBUGS as

```

Model                                     (1)
{                                         (2)
  for (i in 1:N) {                       (3)
    time[i] ~ dweib(r,mu[i]) | (censor[i,]) (4)
    log(mu[i]) <- -r*log(lambda)          (5)
  }                                       (6)
  # Priors:                              (7)
  loglambda ~ dnorm(0, 0.1)              (8)
  lambda <- exp(loglambda)                (9)
  alpha <- -r*log(lambda)                 (10)
  logr ~ dnorm(0, 0.1)                   (11)
  r <- exp(logr)                          (12)
}                                         (13)

```

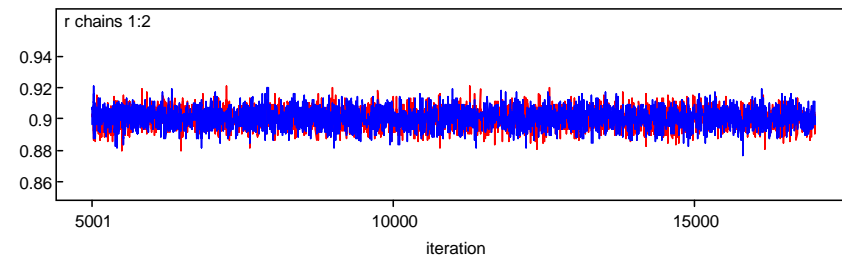
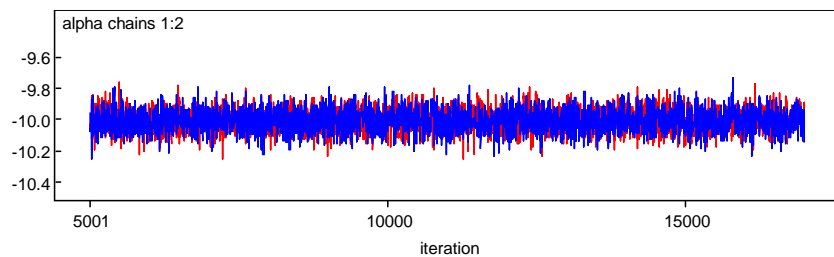
This may be extended to include covariates and random effects. The form of the model including all significant covariates and random effects, as written in WinBUGS, can be found in Appendix 4.

Using the re-parameterised version of the scale parameter, μ , a model containing only an intercept, i.e. $\log(\mu) = \alpha$, was fitted to both simulated datasets, i.e. with no censored observations and with a high percentage of censored observations. This was done in order to investigate if the correlation between alpha and the shape parameter had been reduced. GHQ-12 score was then added to the model before adding all covariates to fit the full model in order to see what effect adding further covariates to the model would have. Results are displayed in Table 8.16 below. Trace plots for alpha, r and the higher-level variance, σ_u^2 , as well as for the GHQ-12 score regression parameters (where applicable) are displayed in Figures 8.7 and 8.8. Corresponding Gelman-Rubin plots are displayed in Figures 8.9 and 8.10. Trace plots and Gelman-Rubin plots for the other significant covariates in the full model are not displayed here.

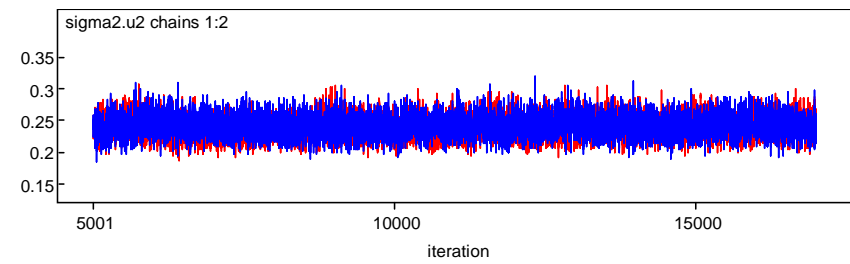
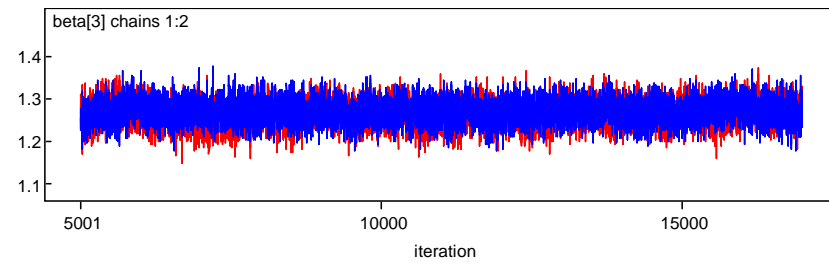
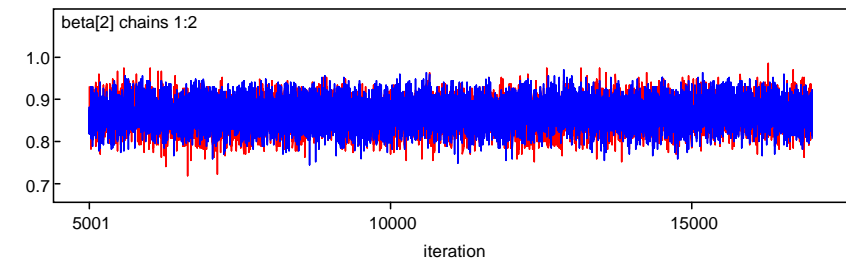
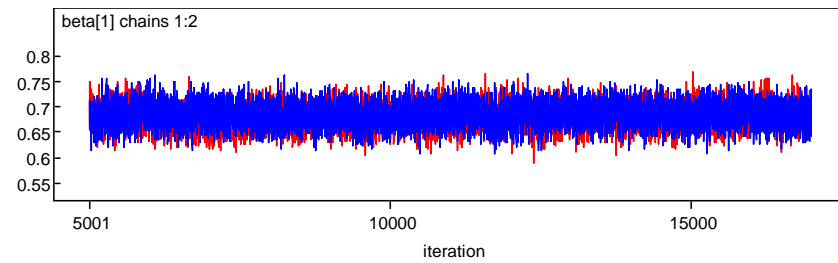
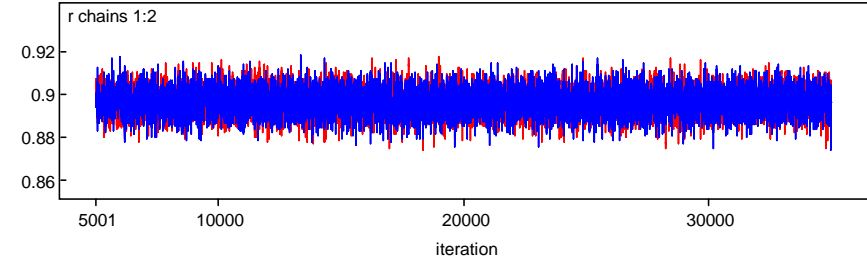
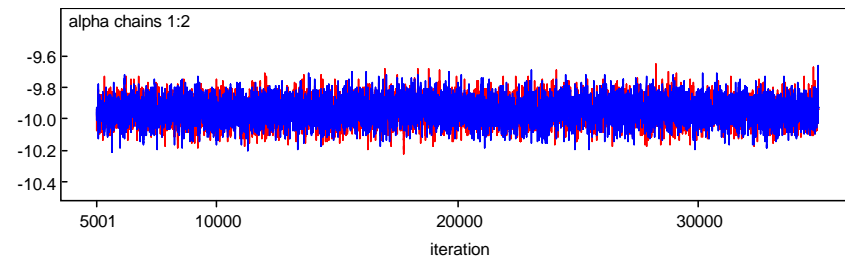
Table 8.16 - Results from re-parameterised model fitted to simulated data

	No Censoring						80% Censoring					
	Intercept		GHQ-12		Full		Intercept		GHQ-12		Full	
	Est.	95%CrI	Est.	95%CrI	Est.	95%CrI	Est.	95%CrI	Est.	95%CrI	Est.	95%CrI
Fixed												
Intercept (α)	-10.0	(-10.14, -9.88)	-9.9	(-10.09, -9.81)	-10.9	(-11.09, -10.76)	-10.5	(-11.1, -9.96)	-10.5	(-10.85, -10.07)	-11.0	(-11.31, -10.71)
GHQ-12 Score												
0			0		0				0		0	
1-2 (β_1)			0.68	(0.64, 0.72)	0.98	(0.93, 1.02)			0.61	(0.47, 0.74)	0.91	(0.80, 1.02)
3-4 (β_2)			0.86	(0.80, 0.92)	1.58	(1.51, 1.64)			0.78	(0.61, 0.95)	1.59	(1.46, 1.71)
5-12 (β_3)			1.27	(1.21, 1.32)	2.84	(2.77, 2.90)			1.23	(1.10, 1.36)	2.82	(2.72, 2.93)
Sex												
Male					0						0	
Female (β_4)					-0.26	(-0.29, -0.23)					-0.28	(-0.35, -0.20)
Age												
16-24					0						0	
25-34 (β_5)					-0.42	(-0.48, -0.35)					-0.50	(-0.62, -0.37)
35-44 (β_6)					0.20	(0.14, 0.26)					0.15	(0.04, 0.27)
45-54 (β_7)					-2.67	(-2.74, -2.60)					-2.71	(-2.93, -2.50)
55-64 (β_8)					-1.43	(-1.50, -1.37)					-1.45	(-1.60, -1.28)
65-74 (β_9)					1.25	(1.17, 1.32)					1.16	(1.02, 1.30)
Marital Status												
Married/cohabiting					0						0	
Other (β_{10})					0.76	(0.73, 0.80)					0.71	(0.64, 0.79)
Receipts of Benefits												
No					0						0	
Yes (β_{11})					1.20	(1.16, 1.24)					1.20	(1.12, 1.28)
Smoking Status												
Non-Smoker					0						0	
Current Smoker (β_{12})					0.70	(0.66, 0.74)					0.63	(0.55, 0.72)
Ex-Smoker (β_{13})					0.02	(-0.02, 0.06)					0.04	(-0.07, 0.14)

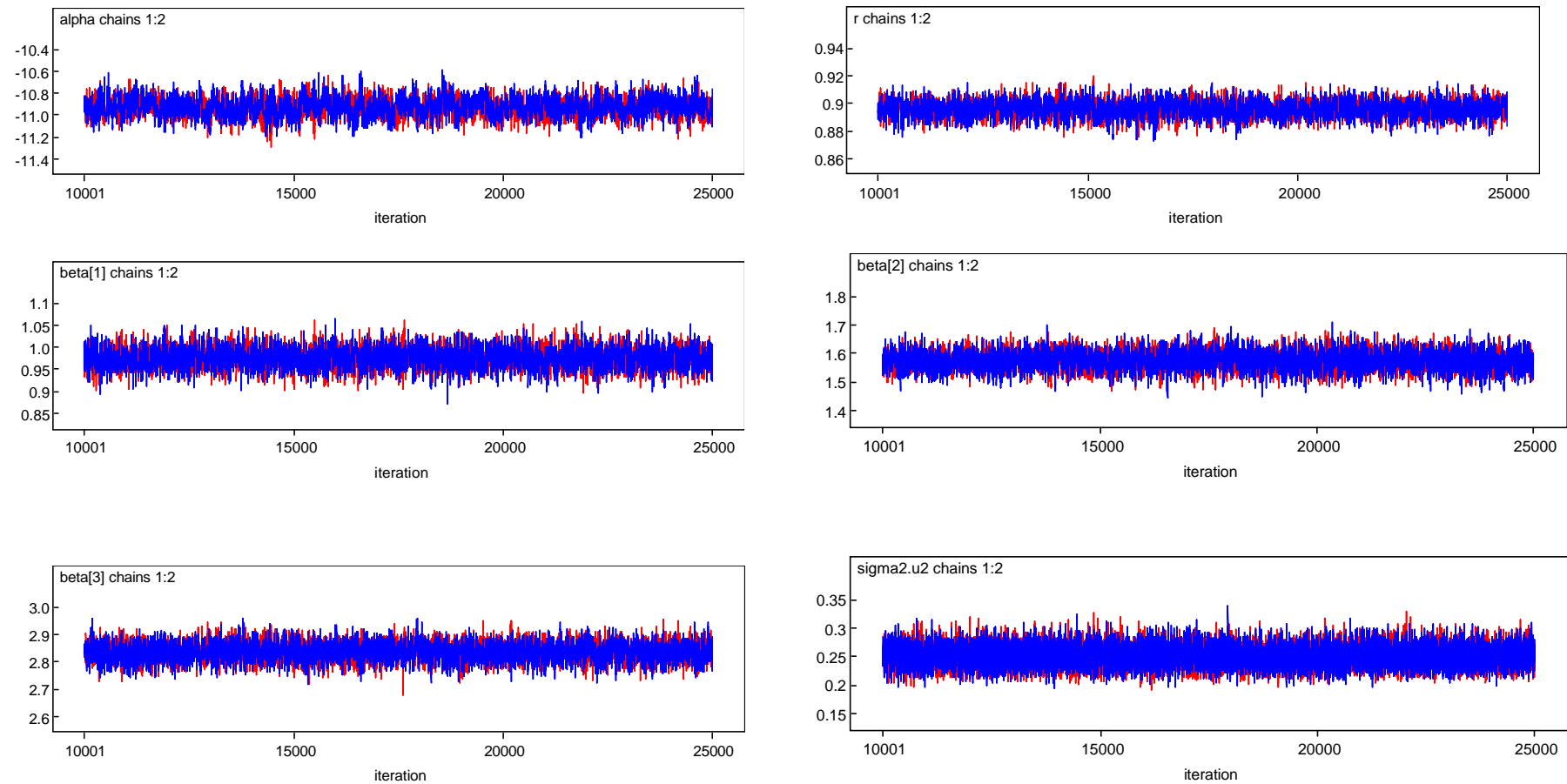
Employment Status						
<i>Full-Time</i>			0			0
<i>Unemployed</i> (β_{14})			0.53 (0.46, 0.61)			0.40 (0.26, 0.55)
<i>Part-Time</i> (β_{15})			-0.64 (-0.68, -0.60)			-0.70 (-0.81, -0.59)
Self-Assessed Health						
<i>Very Good</i>			0			0
<i>Good</i> (β_{16})			1.02 (0.98, 1.06)			0.99 (0.90, 1.09)
<i>Fair</i> (β_{17})			2.86 (2.79, 2.92)			2.86 (2.75, 2.96)
<i>Bad</i> (β_{18})			0.73 (0.61, 0.84)			0.63 (0.34, 0.90)
<i>Very Bad</i> (β_{19})			8.67 (8.44, 8.90)			8.82 (8.51, 9.11)
<i>Shape</i> (r)	0.90 (0.89, 0.91)	0.90 (0.89, 0.91)	0.90 (0.88, 0.91)	0.95 (0.89, 1.03)	0.96 (0.91, 1.01)	0.93 (0.90, 0.96)
Random						
Area Variation(σ_u^2)		0.24 (0.21, 0.27)	0.25 (0.22, 0.29)		0.33 (0.25, 0.43)	0.27 (0.21, 0.33)



Intercept-only model

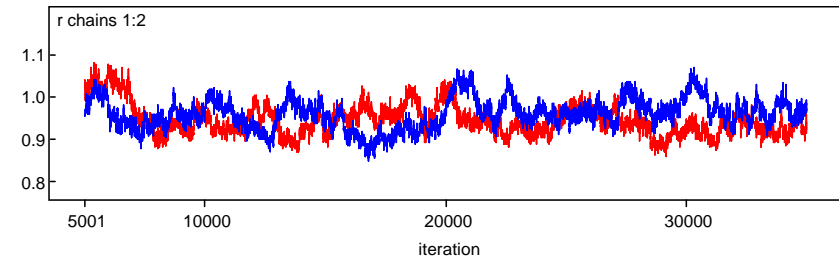
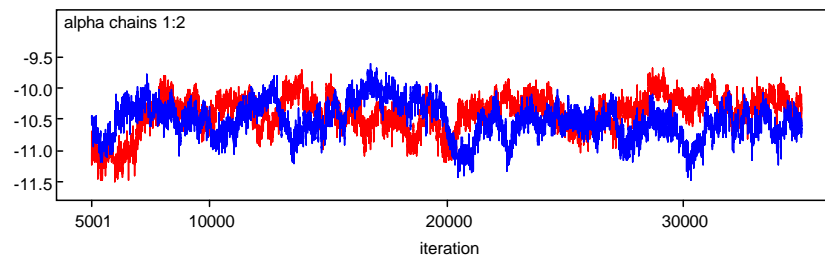


(ii) GHQ-12 model

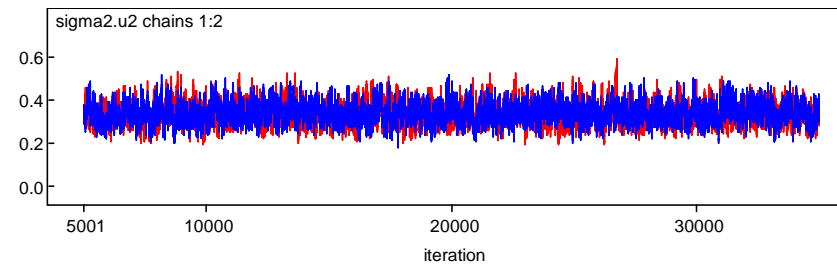
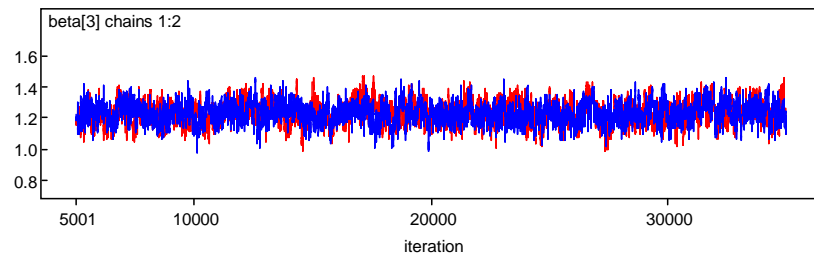
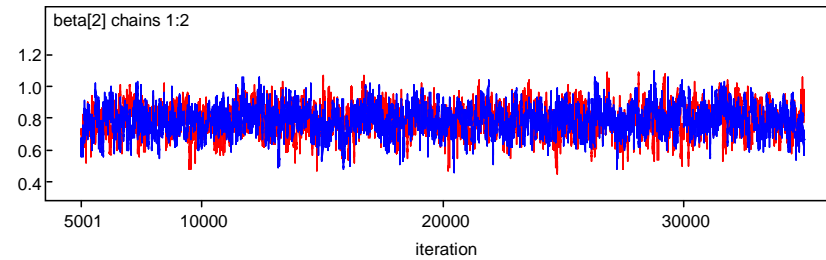
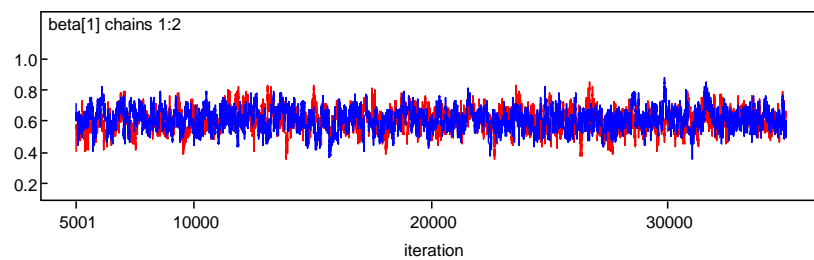
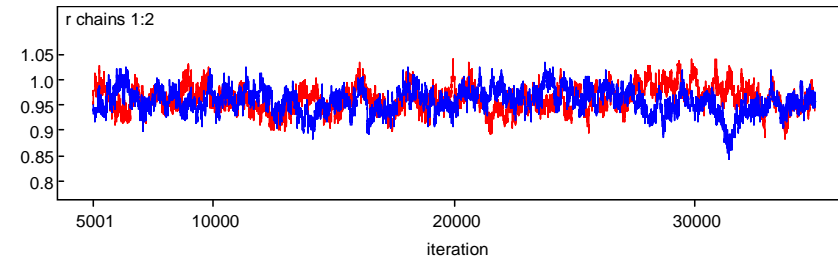
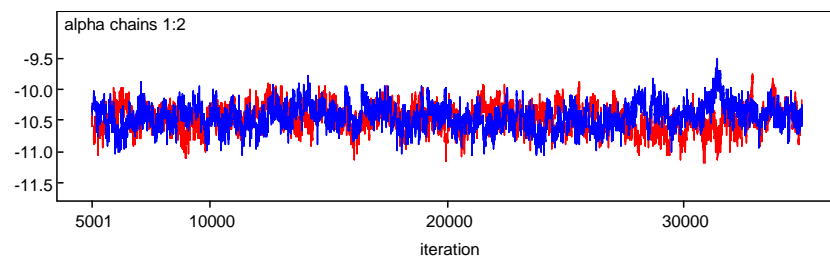


(iii) Full Model

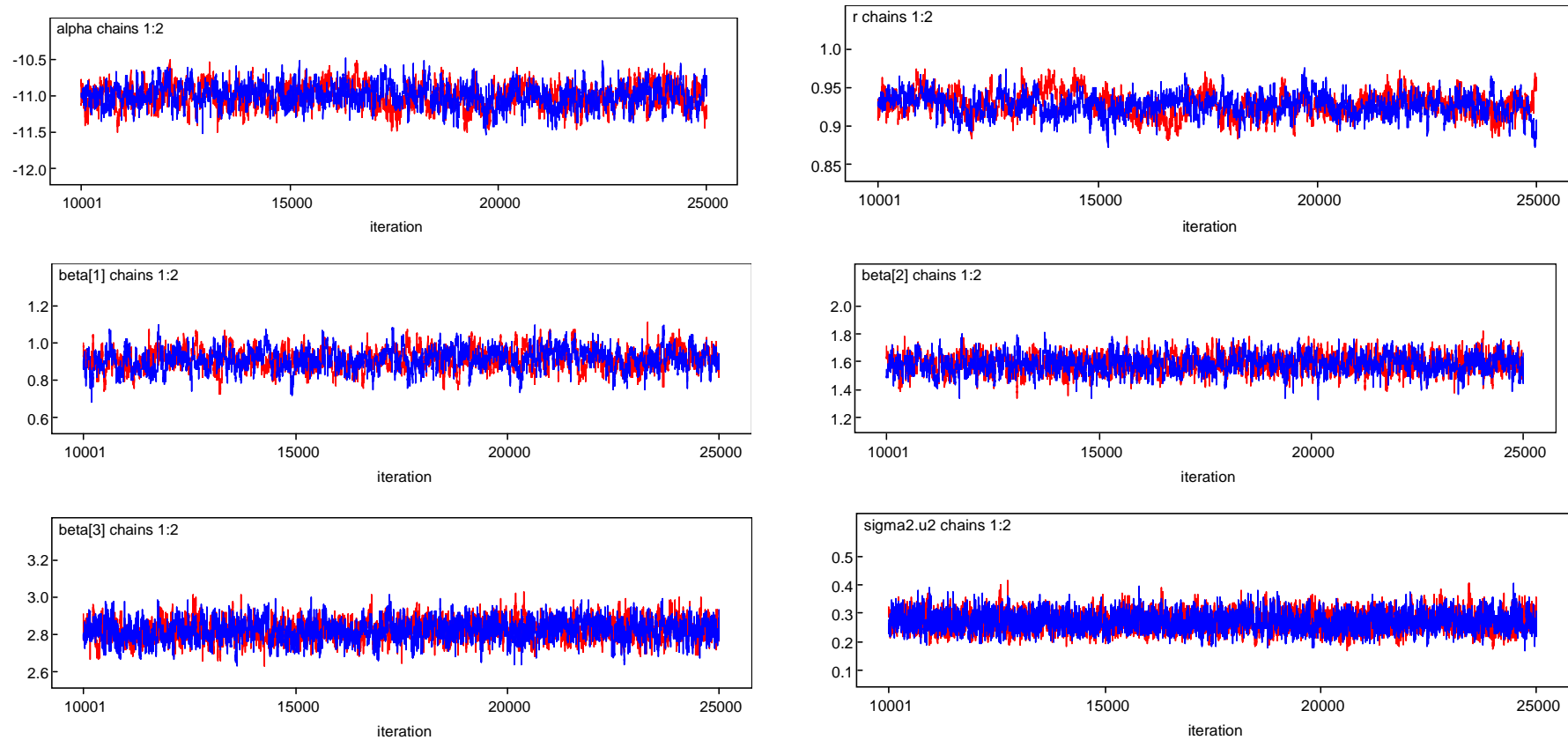
Figure 8.7 - Trace plots for re-parameterised model fitted to simulated dataset with no censoring



(i) Intercept only model

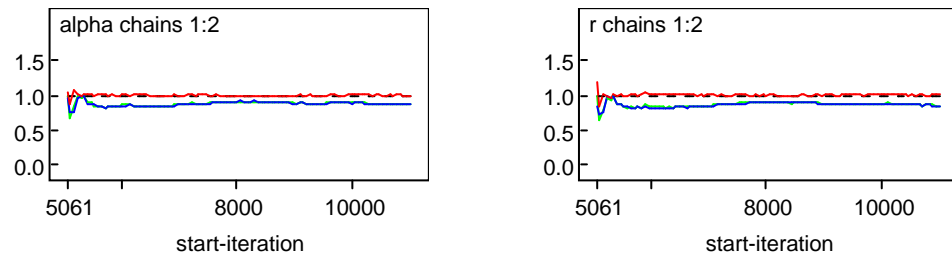


(ii) GHQ-12 model

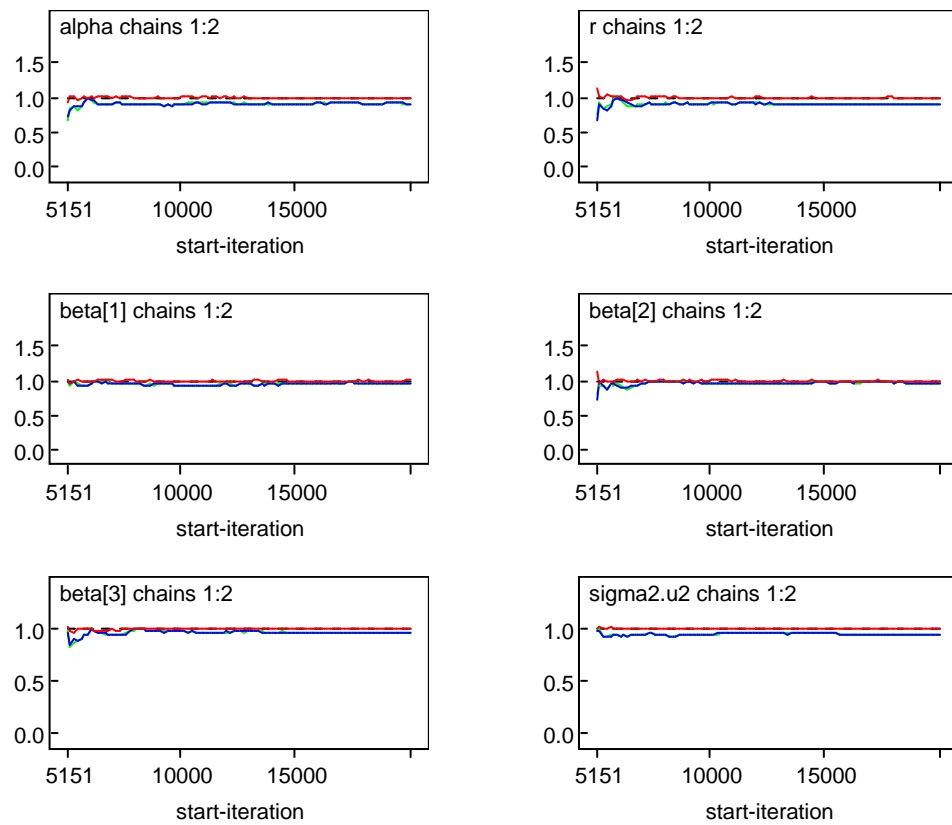


(iii) Full Model

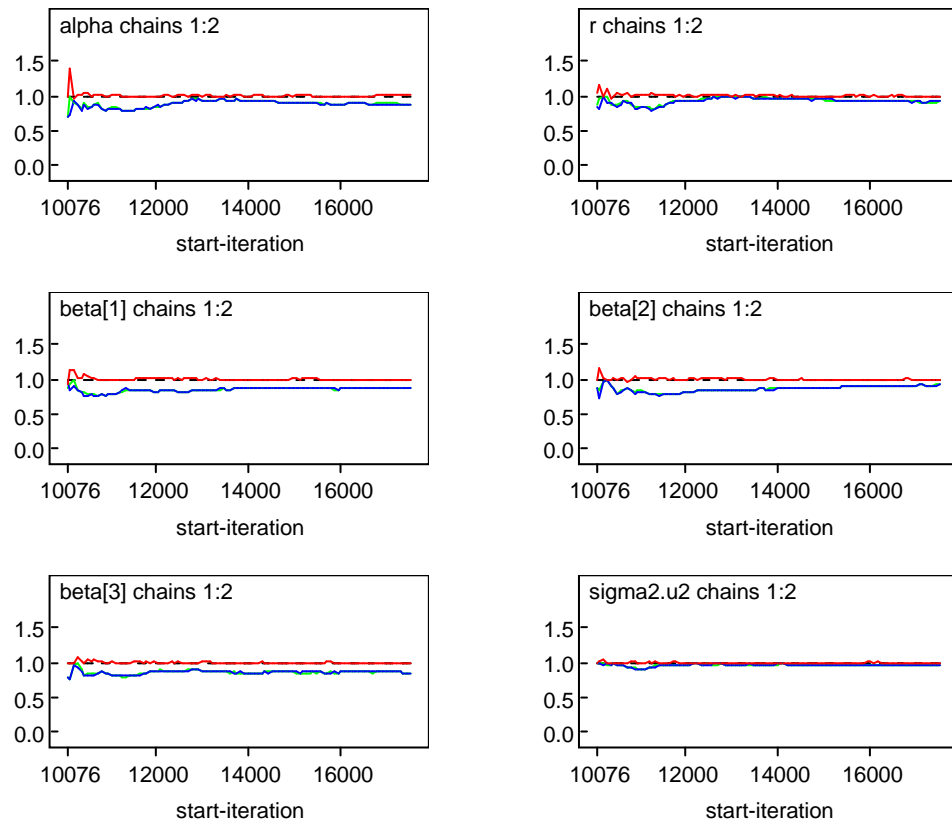
Figure 8.8 - Trace plots for re-parameterised model fitted to simulated dataset with censoring



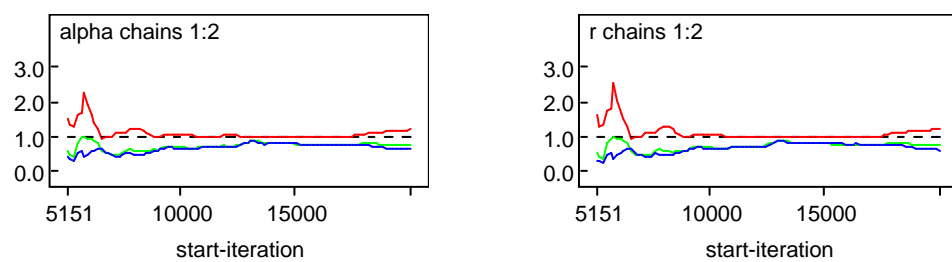
(i) Intercept only model



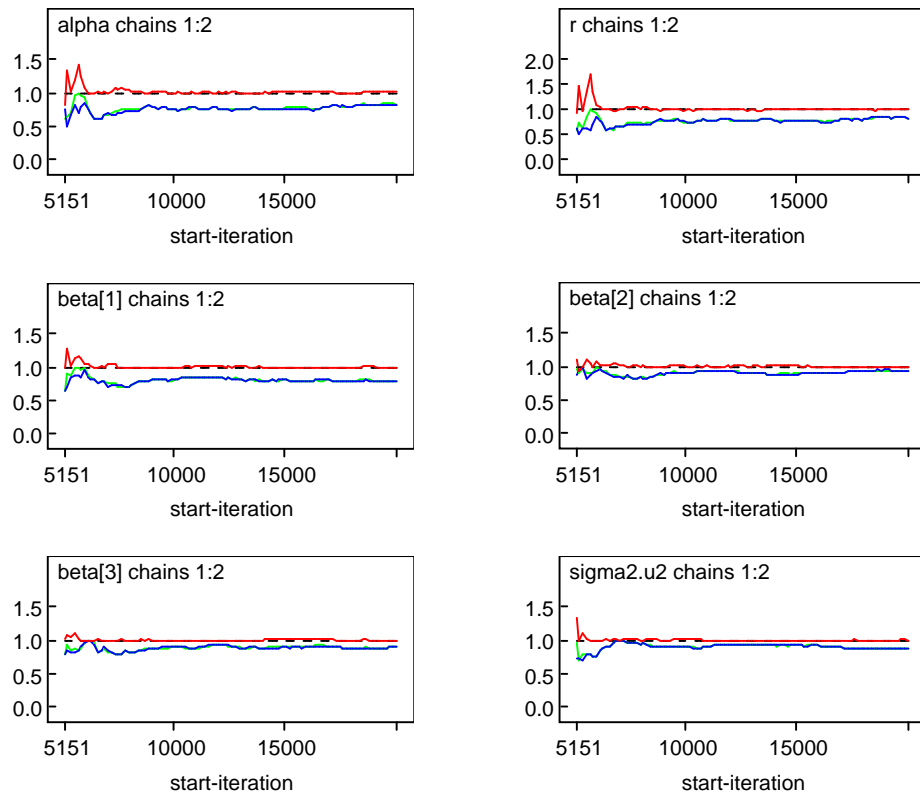
(ii) GHQ-12 model



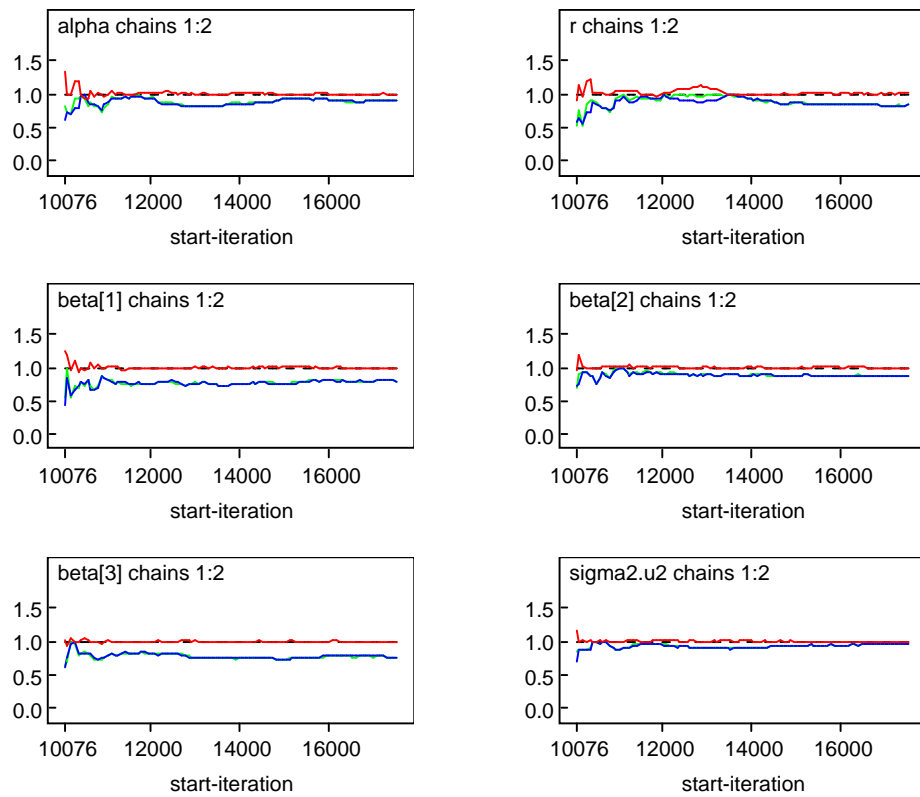
(iii) Full model

Figure 8.9 - Gelman-Rubin plots for re-parameterised model fitted to simulated dataset with no censoring

(i) Intercept only model



(ii) GHQ-12 model



(iii) Full model

Figure 8.10 - Gelman-Rubin plots for re-parameterised model fitted to simulated dataset with censoring

The trace plots in Figures 8.7 and 8.8 can be examined in order to investigate whether re-parameterising the scale parameter, μ , in terms of λ has reduced the correlation in the Markov chains between the intercept, α , and the shape parameter, r . Recall that three models were fitted to both the simulated dataset with no censored observations and the simulated dataset with a high percentage of censored observations: a model including an intercept only; a model including GHQ-12 score and random effects; and a full model including all significant covariates (as determined when fitting the Poisson model displayed in Table 5.3) and random effects.

The trace plots in Figure 8.7 were obtained from fitting the three models described to the simulated dataset with no censored observations. Firstly, from observing the trace plots for the model containing the intercept only (Figure 8.7 (i)), it was clear that the correlation between α and r had been reduced, with the multiple chains for each of these parameters mixing well and having stabilised around the respective sample values of -10 and 0.9. When comparing this to the trace plots obtained from the same model fitted without the re-parameterisation (Figure 8.5), it could be seen that the plots obtained from the model with the re-parameterisation behaved much better than those without and had achieved convergence after a burn-in period of 5000 iterations. This was not the case for the plots from the model without the re-parameterisation. GHQ-12 score and the random effects were then added to this model to see whether or not including any covariates would affect results. All trace plots obtained from fitting the model with the re-parameterisation behaved well. There was no indication of any correlation between α and r , and a burn-in of 5000 iterations had been sufficient to achieve convergence. Finally, all other significant covariates were added to the model including GHQ-12 score. Trace plots for the significant covariates, other than GHQ-12 score, are not displayed here; however, the multiple chains in the trace plots for all other parameters were mixing well, and there was no evidence of any correlation between α and r .

The trace plots in Figure 8.8 were those obtained from fitting the same three models to the simulated dataset with a high percentage of censored observations. Comparing the trace plots from the model including an intercept only (Figure 8.8 (i)) to the trace plots in Figure 8.5 obtained from fitting the

same model without the re-parameterisation, it could be seen that re-parameterising greatly reduced the correlation between α and r . The multiple chains for both parameters were mixing much better after a burn-in period of 5000 iterations than they had been for the model without the re-parameterisation after the same burn-in period. However, the high percentage of censoring seemed to slightly affect results. When the trace plots from Figure 8.8 (i) were compared to those in 8.7 (i), the multiple chains in the plots in Figure 8.8 (i) were not mixing quite as well. This suggested that a bigger burn-in period may have been required (in the presence of censoring) in order to achieve convergence. The Gelman-Rubin plots for α and r in Figure 8.10 (i) suggested that a burn-in period of at least 12000 iterations may have been required to achieve convergence. GHQ-12 score and the random effects were then added to the re-parameterised model fitted to the simulated dataset with a high percentage of censored observations. Examination of the trace plots obtained from this model (displayed in Figure 8.8 (ii)) showed that the correlation between α and r had been reduced further on addition of GHQ-12 score to the model. The multiple chains for α and r were mixing much better than they had been when the re-parameterised model including only an intercept had been fitted to the same data. Comparing this re-parameterised model (Figure 8.8 (ii)) to the same model fitted to the simulated dataset with no censoring (Figure 8.7 (ii)), suggested that the multiple chains for α and r were not mixing quite as well after the same burn-in period (5000 iterations) in the presence of censoring; however, the difference was minimal. Finally, all significant covariates were added to the re-parameterised model fitted to the simulated dataset with a high percentage of censored observations. The multiple chains in the trace plots for α and r (Figure 8.8 (iii)) were mixing fairly well following a burn-in period of 10000 iterations; however, there was perhaps the suggestion from the Gelman-Rubin plots for this model, displayed in Figure 8.10 (iii), that a burn-in period of 13000 iterations may have been more sufficient for achieving convergence. Censoring appeared to have had a small effect on the results. When the trace plots from this model were compared to the trace plots from the same model fitted to the simulated dataset with no censored observations (Figure 8.7 (iii)); there was some evidence that the multiple chains for α and r , in the presence of censoring, were not behaving as well as when

there were no censored observations after the same burn-in period (10000 iterations).

Parameter estimates obtained from fitting the three models to both the simulated dataset without censoring and the simulated dataset with a high percentage of censoring are displayed in Table 8.16. Recall that the parameter estimates used for creating the simulated dataset (i.e. in the calculation of the scale parameter, μ) were those obtained from fitting the continuous-time Poisson model to the SHeS data (Table 5.3); therefore, parameter estimates when fitting the three (re-parameterised) Weibull models to the simulated datasets should be similar to those in Table 5.3. On inspection of the results in Table 8.16, it can be seen that, when the (re-parameterised) model containing an intercept only and the model which also contained GHQ-12 score were fitted to the simulated dataset without censoring, all parameter estimates were close to the values used in the simulation. Additionally, all 95% credible intervals overlapped the values used in the simulation for each parameter. Apart from the intercept in the GHQ-12-only model, this was also the case when the intercept-only model and model containing GHQ-12 score were fitted to the simulated dataset with the high percentage of censoring. It should be noted that the 95% credible intervals in the models fitted to the simulated dataset with a high percentage of censored observations were wider than those from the models fitted to the simulated dataset with no censoring. The parameter estimate for intercept in the model with GHQ-12 score, however, was smaller than expected (-10.5 as opposed to -10), and the 95% credible interval did not overlap -10. When fitting the models with all significant covariates to both simulated datasets (i.e. no censoring and a high percentage of censoring), parameter estimates for most of the covariates were not close to those used when creating the simulated dataset (i.e. obtained from model B3 in Table 5.3), and the 95% credible intervals did not contain these respective values.

To summarise, it appears that re-parameterising the scale parameter in the Weibull model reduced the correlation in the Markov chains between the intercept, α , and the shape parameter, r . This meant that the burn-in period required to achieve convergence using the re-parameterised model was shorter than that required for the model without the re-parameterisation. Hence, the re-parameterised model could be estimated in a shorter time. Fitting models to

simulated datasets with both no censored observations and a high percentage of censored observations revealed that a high percentage of censoring only had a minimal effect on the results and computing time. Thus, it was of interest to go on to fit the re-parameterised model to the actual SHeS dataset, a dataset which contained a high percentage of censored observations, to discover whether or not the re-parameterisation would work with the real dataset.

8.3.4.1 Fitting the Re-parameterised Model to the Scottish Dataset

This section displays results obtained from fitting the re-parameterised model to the Scottish Health Survey dataset. Recall that the purpose of the re-parameterised model was to reduce the correlation in the Markov chains between the intercept parameter, α , and the shape parameter, r , in order to reduce the number of iterations required, hence speeding up computing time. Parameter estimates obtained from fitting a model containing GHQ-12 score only, and a model containing all significant covariates, are presented in Table 8.17. The respective trace plots and Gelman-Rubin plots are given in Figures 8.11 and 8.12 and Figures 8.13 and 8.14. Note that only trace plots and Gelman-Rubin plots for the intercept, GHQ-12 regression parameters, shape parameter and higher level variance, σ_u^2 , are presented. Plots for all other covariates are not included here.

Table 8.17 - Results from Weibull model with re-parameterisation

	GHQ-12 Only		Full Model	
	Estimate	Credible Interval	Estimate	Credible Interval
Fixed				
Intercept (α)	-12.54	(-13.9, -11.52)	-12.39	(-13.88, -11.19)
GHQ-12 Score				
0	0.000		0.000	
1-2 (β_1)	0.656	(0.23, 1.05)	0.466	(0.02, 0.91)
3-4 (β_2)	0.888	(0.37, 1.38)	0.554	(0.01, 1.08)
5-12 (β_3)	1.307	(0.90, 1.72)	0.743	(0.31, 1.16)
Sex				
Male			0.000	
Female (β_4)			-0.184	(-0.50, 0.17)
Age				
16-24			0.000	
25-34 (β_5)			-0.309	(-0.80, 0.33)
35-44 (β_6)			-0.013	(-0.52, 0.53)
45-54 (β_7)			-0.752	(-1.52, -0.15)
55-64 (β_8)			-0.333	(-0.90, 0.25)
65-74 (β_9)			0.149	(-0.64, 0.85)
Marital Status				
Married/cohabiting			0.000	
Other (β_{10})			0.370	(0.01, 0.71)
Receipts of Benefits				
No			0.000	
Yes (β_{11})			0.635	(0.24, 1.00)
Smoking Status				
Non-Smoker			0.000	
Current Smoker (β_{12})			0.695	(0.29, 1.10)
Ex-Smoker (β_{13})			-0.040	(-0.71, 0.57)
Employment Status				
Full-Time			0.000	
Unemployed (β_{14})			0.477	(-0.06, 0.98)
Part-Time (β_{15})			-0.293	(-0.76, 0.17)
Self-Assessed Health				
Very Good			0.000	
Good (β_{16})			0.422	(-0.002, 0.87)
Fair (β_{17})			0.848	(0.38, 1.28)
Bad (β_{18})			-0.084	(-1.35, 0.91)
Very Bad (β_{19})			1.67	(0.68, 2.54)
Shape (r)	0.924	(0.81, 0.98)	0.823	(0.72, 0.96)
Random				
Area Variation(σ_u^2)	0.213	(0.0001, 0.716)	0.244	(0.002, 0.75)

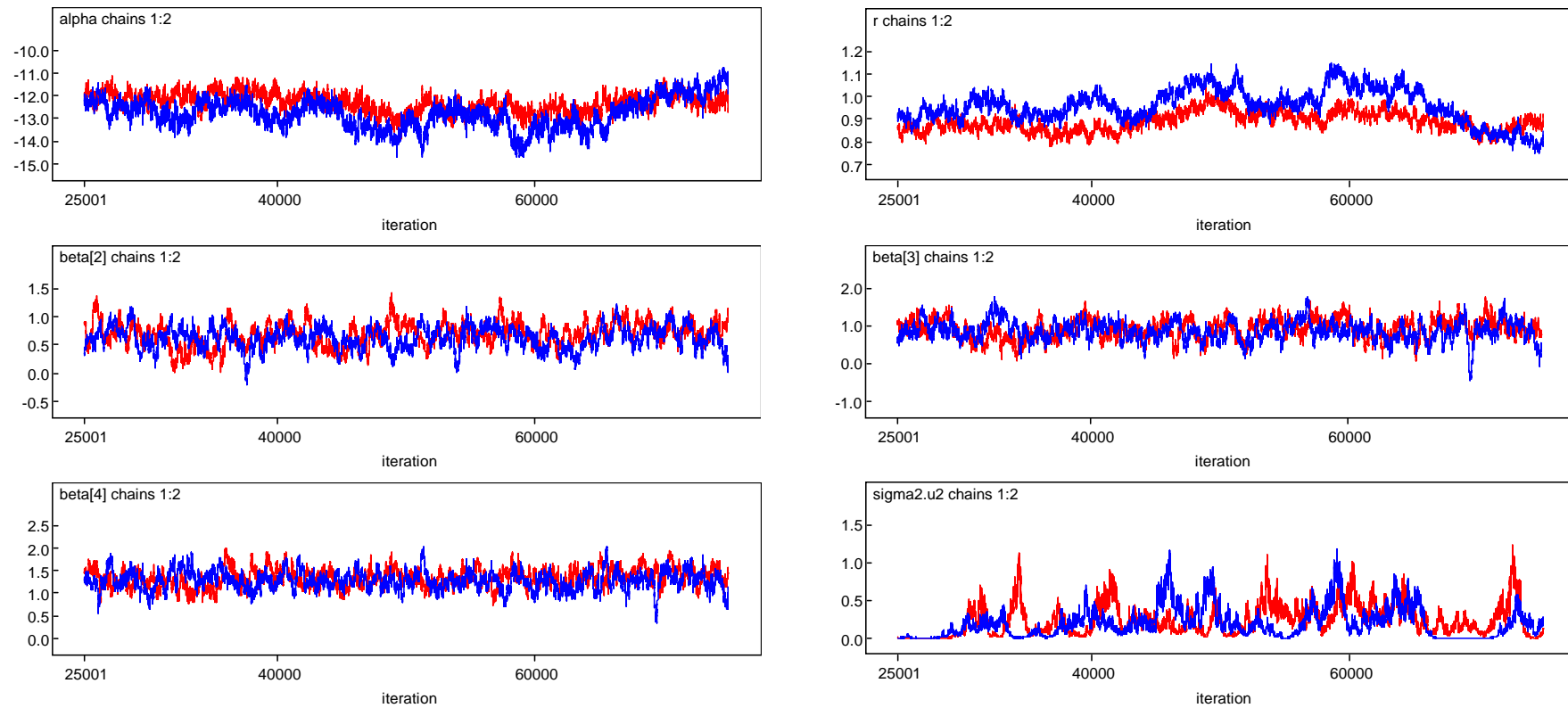


Figure 8.11 - Trace plots for re-parameterised GHQ-12 model

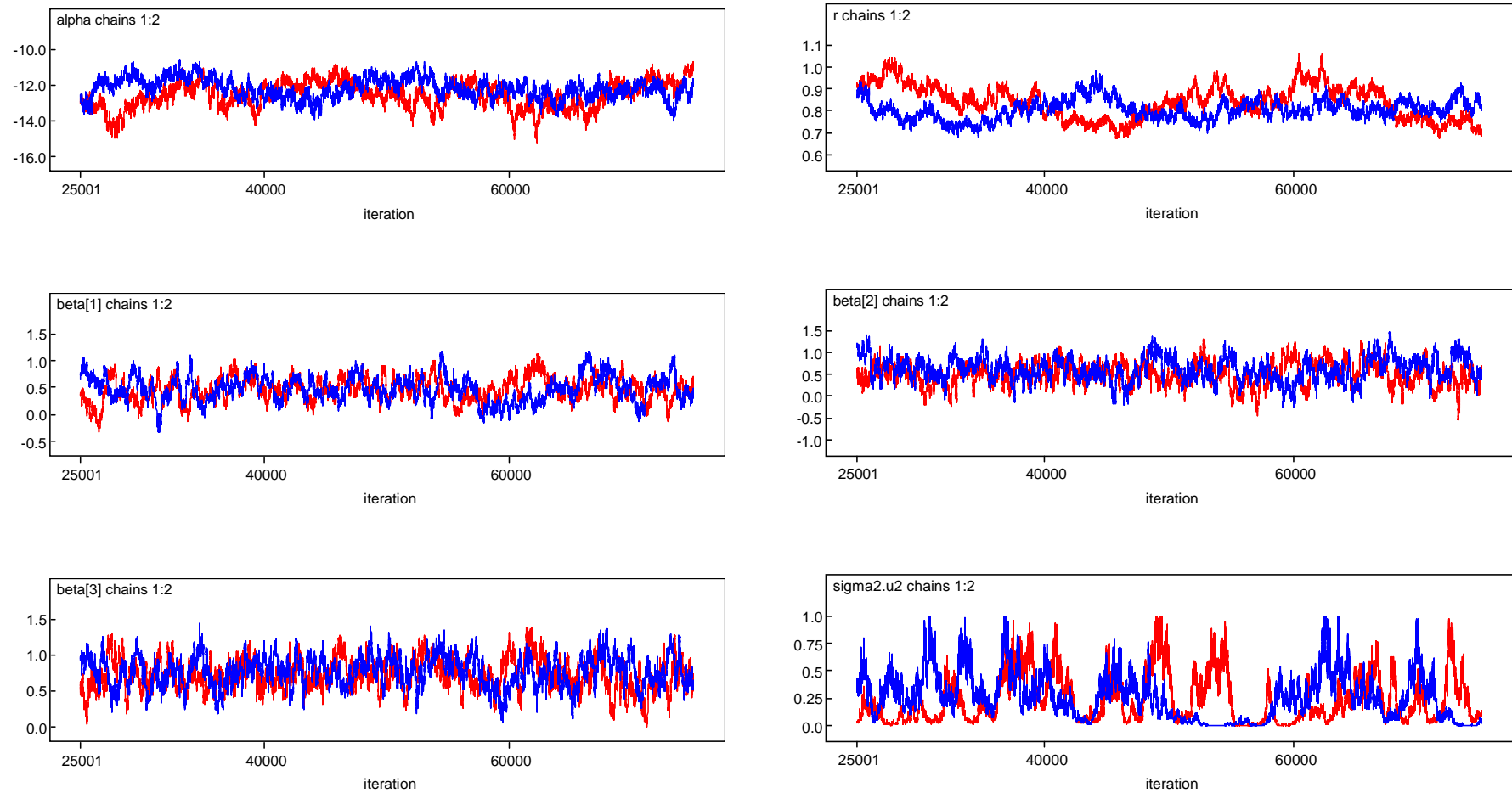


Figure 8.12 - Trace plots for re-parameterised full model

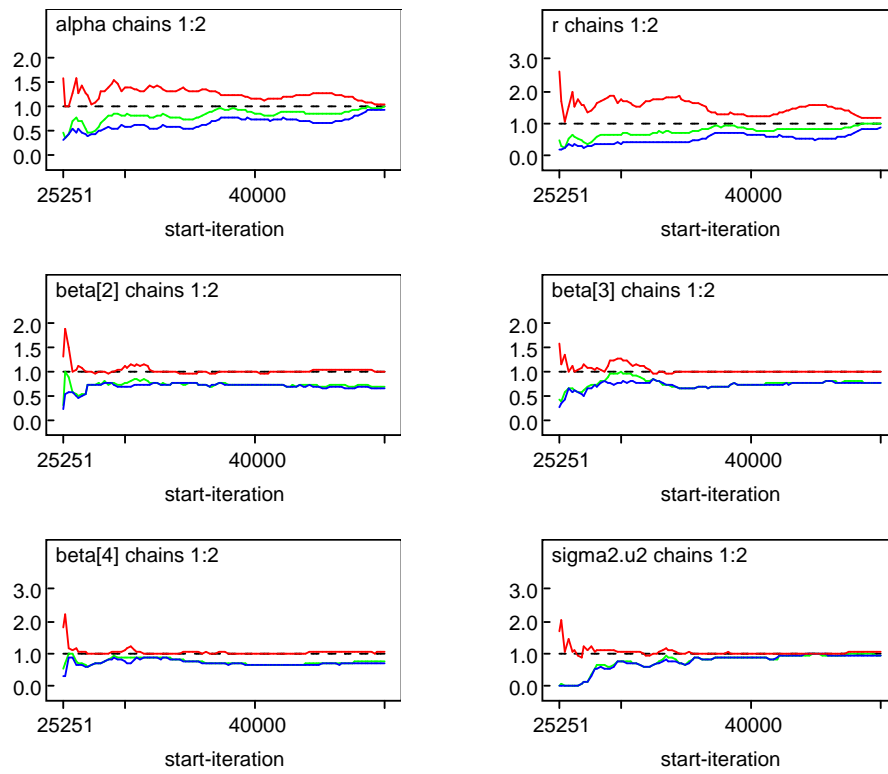


Figure 8.13 - Gelman-Rubin plots for re-parameterised GHQ-12 model

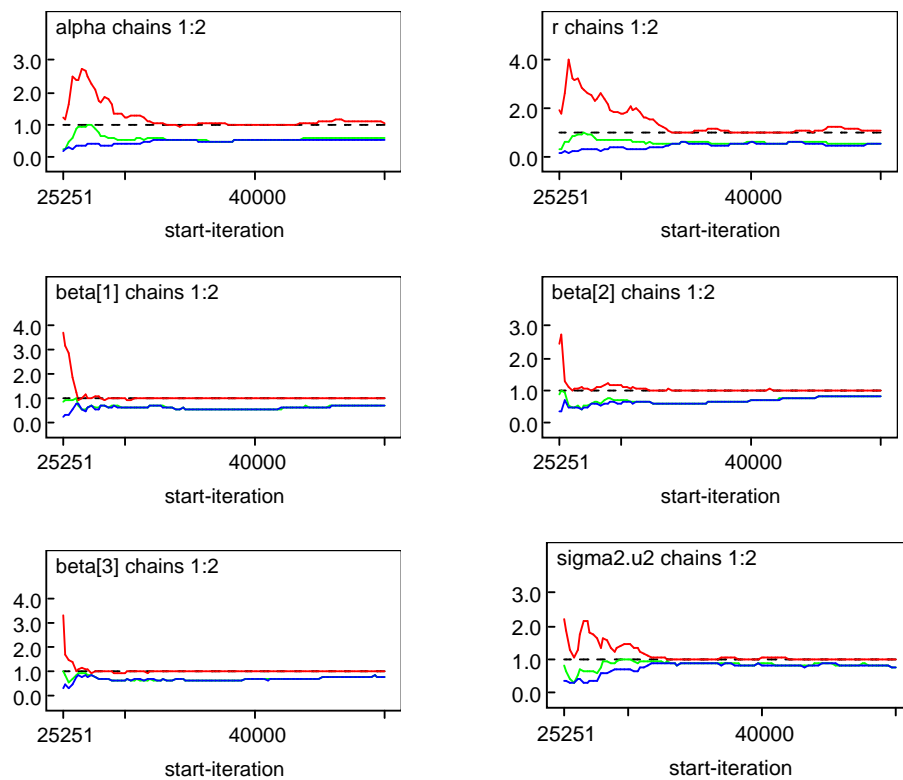


Figure 8.14 - Gelman-Rubin plots for re-parameterised full model

Parameter estimates displayed in Table 8.17 for both the GHQ-12 model and the full model were obtained from running 50000 iterations following a burn-in period of 25000 iterations. From examination of the trace plots in Figures 8.11 and 8.12, and comparing them to the trace plots in Figures 8.7 and 8.8, it can be seen that the re-parameterisation did not perform as well when fitting the model to the real SHeS dataset as it did with the simulated datasets. There still appeared to be correlation in the multiple chains for the intercept and shape parameter even when using the re-parameterised model. Although the multiple chains did appear to be mixing better than they had been without the re-parameterisation (Figures 8.1 and 8.3), this may just have been a result of running more iterations. However, for the full model with and without the re-parameterisation, the burn-in period and the number of iterations after burn-in were the same. The trace plots for the intercept and shape parameter were mixing better in Figure 8.12 than in Figure 8.2; this would support the use of the re-parameterised model. Trace plots for the GHQ-12 regression parameters in Figures 8.11 and 8.12 behaved fairly well, with sufficient mixing of the multiple chains for each; however, the Gelman-Rubin plots for these parameters, displayed in Figures 8.13 and 8.14, suggested that a burn-in period of 35000 iterations may have been more sufficient for achieving convergence. Finally, from observing the trace plot for the higher-level variance, σ_u^2 , it can be seen that the Gibbs sampler was still getting trapped near zero, leading to slow convergence for this parameter. This may be overcome using a parameter expansion scheme which is investigated further in Section 8.3.5.

The parameter estimates obtained from fitting the re-parameterised model to the SHeS dataset (Table 8.17) were compared to those obtained from fitting the model without the re-parameterisation (Table 8.13). Parameter estimates and 95% credible intervals for both the GHQ-12 model and the full model using the re-parameterisation were very similar to those from the original Weibull model. Still perhaps of concern, however, was the 95% credible interval for the higher-level variance, σ_u^2 . Intervals for this parameter in both the GHQ-12 model and the full model were very wide; however, successful implementation of the parameter expansion scheme could possibly lead to more precise interval estimates.

8.3.5 Parameter Expansion in the Weibull Model

Trace plots for the higher-level variance in Figures 8.11 and 8.12 indicated that the Gibbs sampler was getting trapped near zero, hence leading to slow convergence for this parameter. Parameter expansion can be effective when the variance parameter in random-effects models gets trapped near zero. The technique was originally developed to speed up the EM algorithm by Liu et al. [260]; however, it has since also been considered in relation to MCMC sampling and the Gibbs sampler [261]. The parameter expansion technique works by embedding the model of interest in a larger model by including additional redundant parameters. The larger parameter is unidentified; however, the embedded model is still identifiable, and parameters may be extracted [207].

The aim of the parameter expansion technique is to try to reduce the correlation between the random-effects chains and the chain for their variance by introducing an additional parameter that updates the random effects and their variance simultaneously [207]. Each set of residuals is multiplied by an additional parameter, a , say. The parameter expansion technique was adopted for the re-parameterised Weibull model. For a model containing GHQ-12 score only, the re-parameterised Weibull model with parameter expansion was written in WinBUGS as follows:

```

Model (1)
{ (2)
  for (i in 1:N) { (3)
    Time[i] ~ dweib(r,mu[i]) I(Censor[i],) (4)
    log(mu[i]) <- -r*log(lambda[i]) (5)
               + a*v2[AREA[i]] (6)
  } (7)
  #Random effects: (8)
  for (j in 1:624){ (9)
    v2[j] ~ dnorm(0.0, tau.v2) (10)
  } (11)
  # Priors: (12)
  a ~ dunif(0,2) (13)
  loglambda1 ~ dnorm(0, 0.1) (14)
  loglambda2[1] <-0 (15)
  for (k in 2:4){ (16)
    loglambda2[k] ~ dnorm(0, 0.1) (17)
  } (18)
  for (i in 1:N) { (19)
    loglambda[i] <- loglambda1 + loglambda2[GHQ12[i] +1] (20)
    lambda[i] <- exp(loglambda[i]) (21)
  } (22)
  alpha <- -(r*loglambda1) (23)
  beta[1] <- 0 (24)
  beta[2] <- -(r*loglambda2[2]) (25)
  beta[3] <- -(r*loglambda2[3]) (26)
  beta[4] <- -(r*loglambda2[4]) (27)
  # Prior for random effects variance (28)
  sigma.v2~ dunif(0,5) (29)
  sigma2.v2 <- sigma.v2*sigma.v2 (30)
  tau.v2<-1/sigma2.v2 (31)
  z <-a*a (32)
  sigma2.u2 <- z*sigma2.v2 (33)
  logr ~ dnorm(0, 0.1) (34)
  r <-exp(logr) (35)
} (36)

```

The original parameters are thus given by

$$u_j = av_j, \quad \sigma_u^2 = a^2\sigma_v^2,$$

as indicated in lines 6 and 33 of the above WinBUGS code, respectively. Browne [262] discussed that as the ‘a’ parameters multiply both the variance and the residuals, the sampler is given a quick route out of the part of the posterior near the origin. Parameter estimates obtained from fitting this model are displayed in Table 8.18. Trace plots and Gelman-Rubin plots are given in Figures 8.15 - 8.18. As well as GHQ-12 score only, the model was also extended to include all significant covariates, i.e. the full model. Note that, as in previous sections, trace plots and Gelman-Rubin plots are only displayed for the intercept, shape parameter, higher-level variance and the GHQ-12 regression parameters. Plots for the other covariates are not included.

Table 8.18 - Results of re-parameterised Weibull model with variance expansion

	GHQ-12 Only		Full Model	
	Estimate	95% CrI	Estimate	95% CrI
Fixed				
Intercept (α)	-12.47	(-1367, -11.44)	-12.16	(-13.29, -11.05)
GHQ-12 Score				
0	0.000		0.000	
1-2 (β_1)	0.633	(0.22, 1.06)	0.404	(0.02, 0.81)
3-4 (β_2)	0.868	(0.25, 1.38)	0.409	(-0.19, 0.96)
5-12 (β_3)	1.311	(0.87, 1.70)	0.654	(0.17, 1.13)
Sex				
Male			0.000	
Female (β_4)			-0.101	(-0.50, 0.34)
Age				
16-24			0.000	
25-34 (β_5)			-0.265	(-0.79, 0.35)
35-44 (β_6)			0.022	(-0.56, 0.56)
45-54 (β_7)			-0.689	(-1.44, -0.06)
55-64 (β_8)			-0.279	(-0.94, 0.31)
65-74 (β_9)			0.295	(-0.46, 1.02)
Marital Status				
Married/cohabiting			0.000	
Other (β_{10})			0.328	(-0.05, 0.65)
Receipts of Benefits				
No			0.000	
Yes (β_{11})			0.653	(0.20, 1.07)
Smoking Status				
Non-Smoker			0.000	
Current Smoker (β_{12})			0.667	(0.28, 1.06)
Ex-Smoker (β_{13})			-0.078	(-0.67, 0.46)
Employment Status				
Full-Time			0.000	
Unemployed (β_{14})			0.516	(-0.06, 1.05)
Part-Time (β_{15})			-0.352	(-0.83, 0.18)
Self-Assessed Health				
Very Good			0.000	
Good (β_{16})			0.446	(-0.03, 0.18)
Fair (β_{17})			0.895	(0.38, 1.42)
Bad (β_{18})			0.017	(-1.18, 0.98)
Very Bad (β_{19})			1.727	(0.72, 2.58)
Shape (r)	0.917	(0.81, 1.06)	0.794	(0.70, 0.88)
Random				
Area Variation(σ_u^2)	0.183	(0.0003, 0.614)	0.168	(0.0002, 0.64)

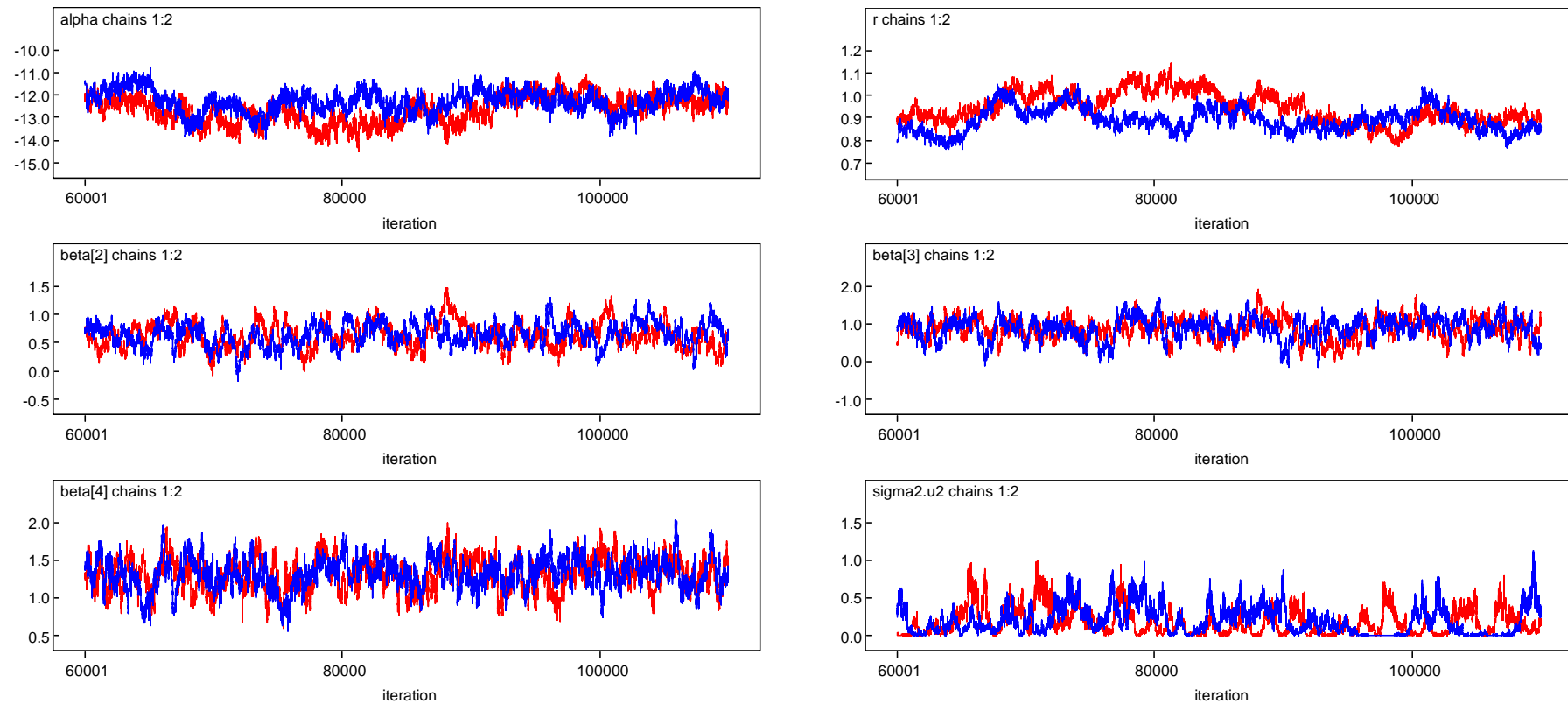


Figure 8.15 - Trace plots for re-parameterised GHQ-12 model with variance expansion

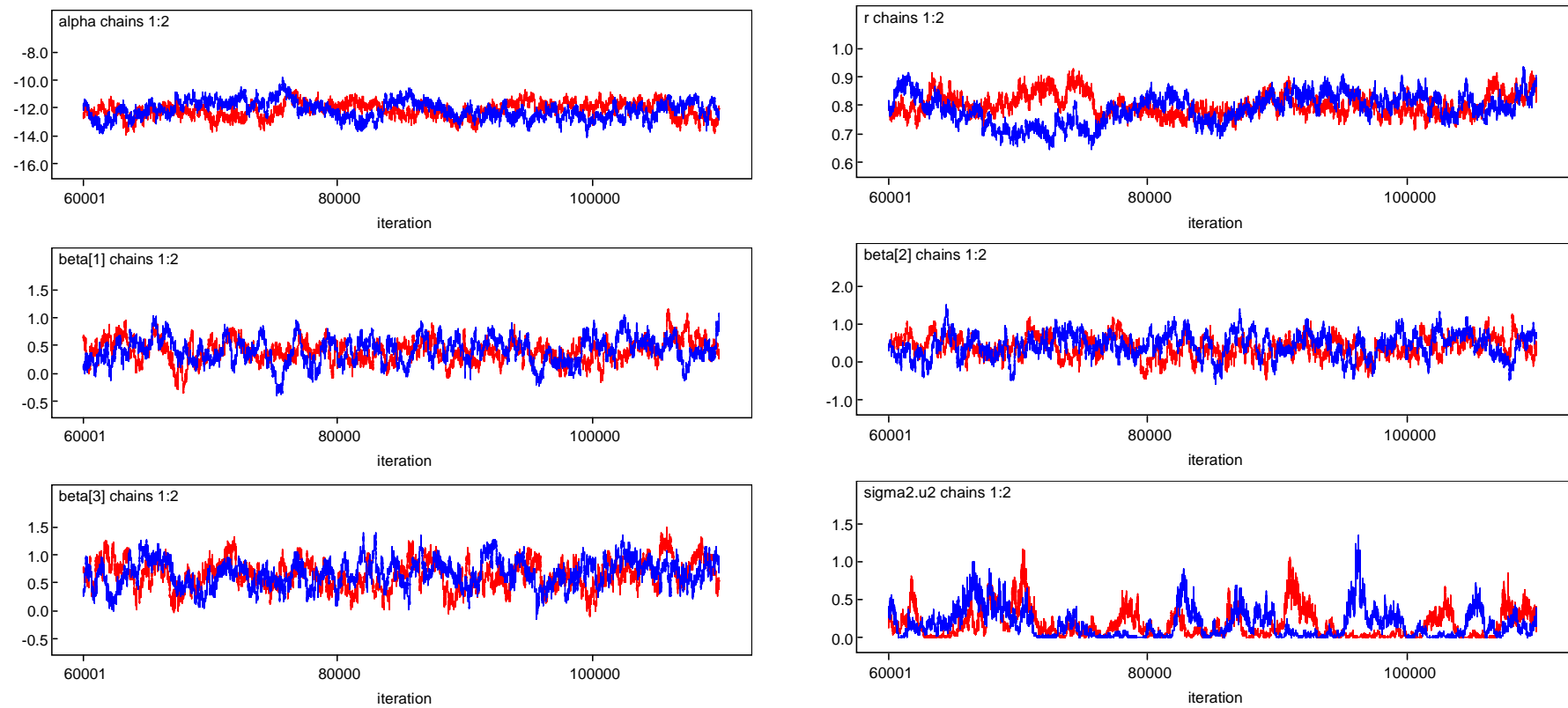


Figure 8.16 - Trace plots for re-parameterised full model with variance expansion

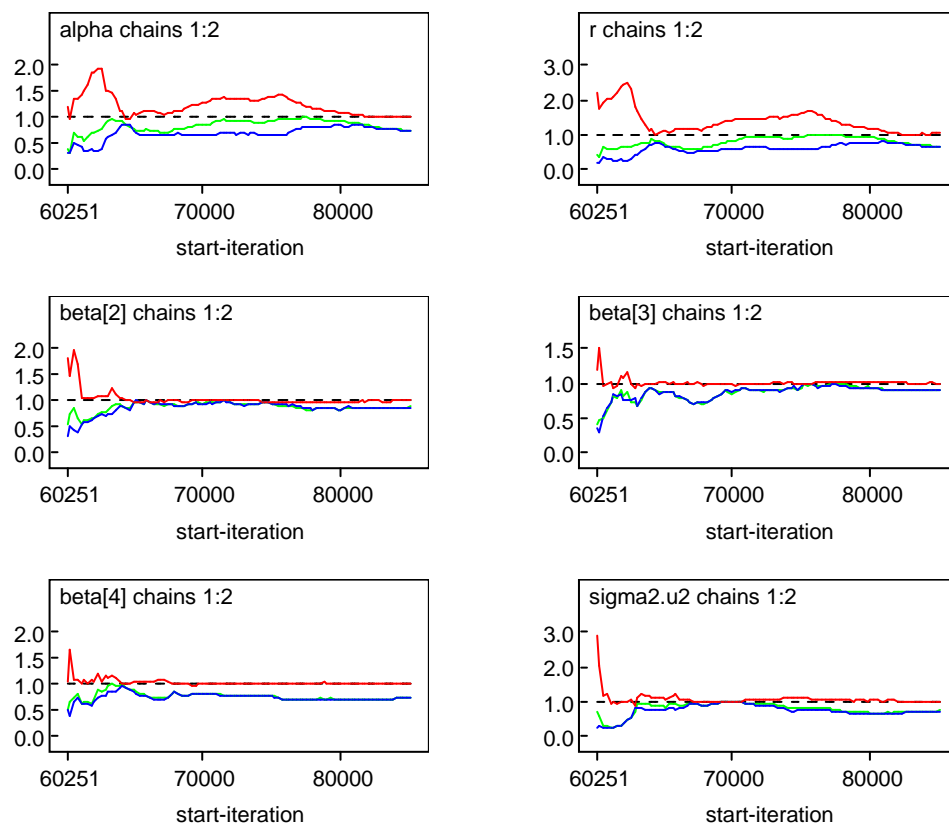


Figure 8.17 - Gelman-Rubin plots for re-parameterised GHQ-12 model with variance expansion

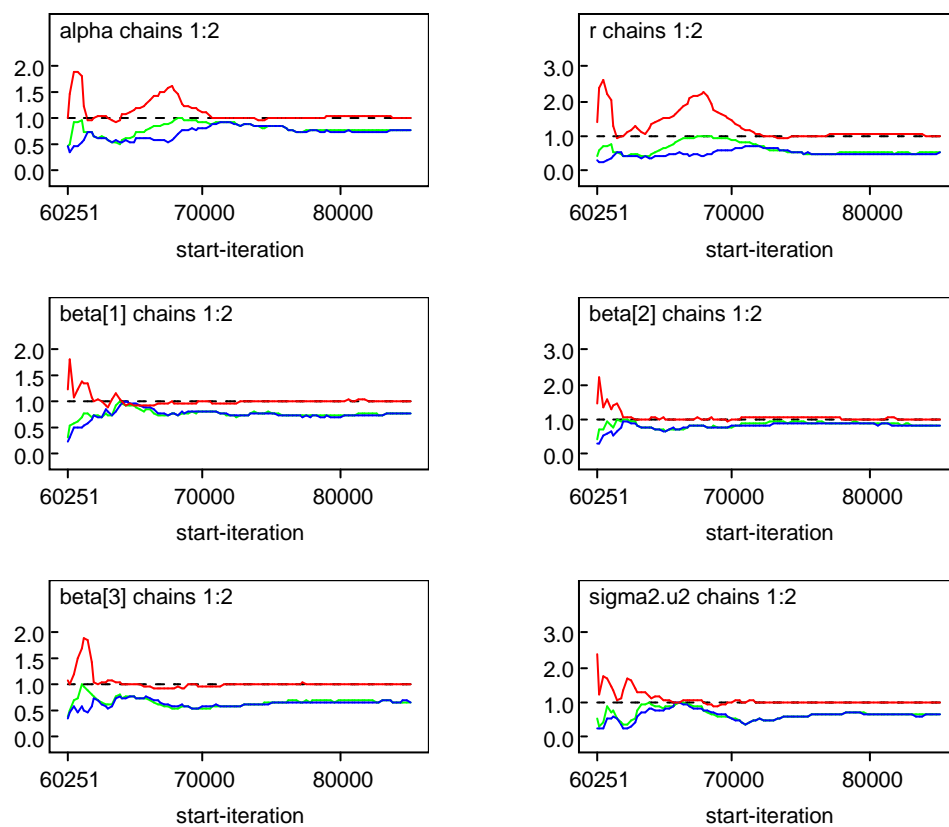


Figure 8.18 - Gelman-Rubin plots for re-parameterised full model with variance expansion

Parameter estimates for both the GHQ-12 model and the full model were obtained after running 50000 iterations, following a burn-in period of 60000 iterations. CPU time was 78269 seconds and 118297 seconds for the GHQ-12 and full model respectively. As the purpose of the parameter expansion was to try to prevent the Gibbs sampler getting trapped near zero for the random-effects variance, it was of most interest to observe the trace plots for this parameter. From looking at the trace plot for the higher-level variance from the GHQ-12 model (Figure 8.15) and comparing this with the trace plots for the same parameter from the original Weibull model (Figure 8.1) and with the re-parameterised Weibull model (Figure 8.11), it can be seen that the parameter expansion technique appeared to have minimal impact on overcoming the problem of the Gibbs sampler getting trapped near zero. The trace plot in Figure 8.15 showed that the Gibbs sampler was still prone to getting trapped at zero even after adopting the parameter expansion technique. The multiple chains were perhaps mixing better when the parameter expansion was used; however, this may just have been a result of having a bigger burn-in period, thus giving the Markov chain a longer time to achieve convergence. The parameter estimate for the higher-level variance was slightly smaller ($= 0.183$) when the parameter expansion was used. This was opposed to estimates of 0.263 and 0.213 for the original Weibull and the re-parameterised Weibull models respectively. The 95% credible interval for this parameter was slightly narrower, also, when the parameter expansion was used compared to the original and re-parameterised Weibull models. However, the interval still covered a wide range of values, perhaps reflecting that convergence had not been achieved before sampling from the posterior distribution.

Similar conclusions were drawn when comparing the trace plot for the full model with the parameter expansion (Figure 8.16) to the trace plots for the original Weibull (Figure 8.2) and re-parameterised Weibull (Figure 8.12) models. Although the multiple chains in the trace plot for the parameter expansion model perhaps appeared to be mixing slightly better, there was still the tendency for the Gibbs sampler to get trapped near zero. Again, from looking at the parameter estimate of the higher-level variance in Table 8.18, it can be seen that the estimate was smaller when the parameter expansion was used ($= 0.168$) when compared with the estimates from the original Weibull (Table 8.13)

and the re-parameterised Weibull (Table 8.17) models. The 95% credible interval was also slightly narrower for the model using the parameter expansion; however, the interval still covered a large range of values.

8.3.6 Summary: Bayesian Frailty Models

Fitting a frailty model using a Bayesian approach in WinBUGS was viewed as a favourable alternative to the Poisson model in MLwiN for fitting continuous-time survival models as it avoided the need for data expansion. This section focussed on fitting frailty models to the SHeS data assuming a Weibull distribution for survival times, and a log-Normal frailty distribution. As MCMC estimation was to be used when fitting the models in WinBUGS via a Bayesian approach, as opposed to PQL estimation in MLwiN, it was necessary to check that both methods of estimation would produce similar results. This was done by re-fitting the continuous-time Poisson model in WinBUGS and using MCMC estimation to estimate model parameters. Similar parameter estimates were obtained from fitting the same model with the two different methods of estimation, meaning that, when the Weibull model was fitted in WinBUGS using MCMC estimation, parameter estimates could be compared to those from models using PQL estimation.

The Weibull model with log-Normal frailty was then fitted to the SHeS dataset. A model containing only GHQ-12 score and another containing all of the significant covariates were fitted, and results were compared to those obtained from fitting the original continuous-time Poisson model (Table 5.3). Although parameter estimates for the GHQ-12 model and the full model from fitting the Weibull and the Poisson models were similar, there were some problems with convergence of the Markov chains when estimating the Weibull models. The two main issues were that the Markov chains for the intercept and the shape parameter of the Weibull distribution appeared to be correlated. The multiple chains for these parameters did not appear to be mixing well, indicating poor convergence. Furthermore, the multiple chains for the higher-level variance were not mixing well, and the Gibbs sampler was prone to getting trapped near zero. It was thought that the high percentage of censored observations in the SHeS dataset

may have been the root of these problems; therefore, to investigate this notion further, a simulation study was carried out.

Two datasets were created in the simulation study - one with no censored observations, and another with a percentage of censored observations similar to that of the actual SHeS dataset (approx. 99%). The apparent correlation between the intercept and shape parameter was the first issue to be considered. Results from fitting the Weibull model to the simulated datasets suggested that a high percentage of censoring was not the main cause of the problem. As the problem could not be attributed entirely to the level of censoring, a re-parameterised version of the Weibull model was considered as a possible way of reducing the correlation between these parameters. It was hoped that this would speed up computing time by reducing the number of iterations required (Section 8.3.4). By re-parameterising the scale parameter of the Weibull distribution, the correlation between the multiple chains of the intercept and shape parameter was greatly reduced, even when there was a high percentage of censored observations.

As re-parameterising the Weibull model seemed to reduce the correlation between the intercept and the shape parameter when fitting models to the simulated datasets, it was then of interest to try fitting this model to the actual SHeS dataset. The re-parameterised model appeared to work just as well when fitted to the SHeS dataset; however, there were still problems with the higher-level variance in that it was still prone to getting trapped near zero. This problem had not existed when fitting models to the simulated datasets.

A parameter expansion technique was adopted to try and overcome this problem (Section 8.3.5). Parameter expansion has been shown to be effective when the variance parameter in random-effects models gets trapped near zero. When applied in the Weibull model fitted to the SHeS dataset, however, this technique did not appear to have much impact on overcoming the problem of the Gibbs sampler getting trapped near zero. Instead, a possible solution would have been to run more iterations; however, this is not a computationally efficient method, particularly for a large dataset.

8.4 Chapter Summary

This chapter presented results obtained from fitting the alternative models, discussed in Chapter 7, to the Scottish Health Survey dataset. Recall that three methods were being investigated as an alternative to fitting continuous-time Poisson models in MLwiN, namely, discrete-time models, grouping according to covariates, and fitting multilevel survival models in WinBUGS using a Bayesian approach. As fitting the continuous-time Poisson model in MLwiN required the use of a person-period dataset, the original dataset, which must be expanded in order to create the person-period dataset, can often become very large. This can be problematic if the dataset was large to begin with, as is often the case with survey data used in the field of public health. Therefore, the three methods named above were considered as a solution to overcome the problems associated with fitting continuous-time models, in particular by allowing the size of the dataset after expansion to be reduced. This section will assess the adequacy of these three methods as possible alternatives to continuous-time models based on the following criteria: the percentage reduction in the expanded dataset for the continuous-time model; the similarity of the parameter estimates when compared with the original continuous-time model; and, finally, how easy they were to implement.

The first alternative method to be considered involved defining different risk sets so that, instead of treating time as a continuous variable, it was divided into short intervals meaning discrete-time models could then be used. The discrete intervals could be either of equal length or of varying length, defined according to when events occurred. Both approaches were considered when testing this method on the SHeS dataset. Firstly, intervals of equal length were considered, where the follow-up time was divided into years and, secondly, intervals of varying length were considered. Dividing the follow-up time into year-long intervals created 9 risk sets, as opposed to 136 risk sets when time was treated as a continuous variable. Having only 9 risk sets meant that the size of the expanded dataset was 110643 (observations within individuals). This was a reduction of approximately 94% of the original dataset, which consisted of just fewer than 1.9 million observations within individuals following expansion. When intervals of varying length were created according to when events occurred,

time was divided such that just 4 risk sets resulted. With only 4 risk sets, the size of the person-period dataset was then 54580, a 97% reduction of the expanded dataset from when time was continuous. Parameter estimates of the fixed effects, obtained from fitting discrete-time models to the expanded datasets containing 4 risk sets and 9 risk sets, were very similar to those obtained from fitting continuous-time models. There were some differences in the estimates of the random effects when time was grouped into longer discrete intervals to create the 4 risk sets. A possible explanation for this was given in Section 8.1.2. Discrete-time models were easy to implement since standard methods for fitting discrete response data, such as logistic regression, could be used to fit them after some restructuring of the data so that the response variable was binary.

The second method considered was the ‘grouping according to covariates’ method. As all individuals within the same postcode sector with the same values for covariates included in a particular model are at risk at the same time, their data could be aggregated so that just one line of data represented all such individuals. Time could be treated as a continuous or a discrete variable, meaning either Poisson or logistic regression models could be used. As a new dataset had to be created each time a covariate was added to the model, the sizes of the person-period datasets for fitting the three different models, i.e. the GHQ-12 only model, the full model without self-assessed general health and the full model with self-assessed general health were all different. When time was treated as continuous, the percentage reduction of the original expanded dataset ranged from 4% to 84% depending on the number of covariates in the model. When time was treated as discrete and intervals varied in length (i.e. were defined in the way that created 4 risk sets), the percentage reduction in the original continuous-time expanded dataset ranged from 97% to 99.5%. Having fewer covariates in the model led to a greater percentage reduction in the original continuous-time person-period dataset consisting of around 1.9 million observations within individuals. Parameter estimates for the fixed and random effects obtained from fitting continuous-time models to the aggregated dataset, i.e. the dataset which had been grouped according to postcode sectors and covariates, were identical. Although estimates of the fixed effects obtained from fitting discrete-time models to the aggregated dataset were similar to

those of the original continuous-time Poisson model and also to those of the discrete-time model fitted to the dataset without aggregation, there were some differences in the estimates of the random effects. However, the differences were not especially large and 95% confidence intervals (not displayed) for the higher-level variance from the discrete-time model fitted to the aggregated dataset contained the estimate of the higher-level variance from the original Poisson model (0.255 and 0.246 for the GHQ-12 only and full models respectively).

The grouping according to covariates method was not the easiest method to implement. The aggregated dataset had to be created using a specially written macro, and had to be re-created each time the covariates in the model changed; hence the use of this method would not be recommended for model selection. The number of covariates to be grouped on and the number of individuals within postcode sectors also affected how effective this method was at reducing the size of the original continuous-time person-period dataset. For a postcode sector consisting of a large number of individuals, there was a greater chance that there would be more individuals within that postcode sector sharing the same values of covariates and vice versa. This then leads to a bigger (smaller) reduction in the size of the expanded dataset as there would be more (fewer) individuals within a postcode sector that could be grouped together by the values of their covariates. Ultimately, however, regardless of the number of individuals in each postcode sector, the number of individuals with identical covariates would become smaller as the number of covariates to be grouped on increased.

Risk factors measured on a continuous scale may also be problematic when using the grouping according to covariates method. For example, consider an individual from a defined postcode sector aged 30 years with a GHQ-12 score of 3, where both age and GHQ-12 score are measured on a continuous scale. If there are a large number of individuals within the defined postcode sector, then it may be more likely that other individuals will share the exact age of 30 years and GHQ-12 score of 3 than if there were a small number of individuals within the postcode sector. However, regardless of how many individuals there are within a postcode sector, the number of individuals sharing exact values for continuous risk factors will decrease as the number of continuous variables to be

grouped on increases, even more so than when risk factors are recorded on a discrete scale. Therefore, this method may not be particularly effective at reducing the size of the continuous-time person-period dataset if there are a large number of covariates to be grouped on, especially if many of them are continuous.

The final method to be considered involved fitting Bayesian shared frailty models in WinBUGS, assuming a log-Normal distribution for the frailties. The survival times were assumed to follow a Weibull distribution. An advantage of using this approach was that the data did not need to be expanded to fit the Weibull models; therefore, the size of the dataset for this approach remained at 15305 individuals (nested within 624 postcode sectors). Parameter estimates were obtained via MCMC using Gibbs sampling. It was shown that parameter estimates obtained from the Weibull model could be interpreted as hazard ratios; hence they were comparable with those obtained from fitting the continuous-time Poisson model. Parameter estimates of fixed and random effects obtained from the Weibull model were very similar to those obtained from the Poisson model; however, 95% credible intervals for the random-effects variance were very large, a possible result of poor mixing of the Markov chains for this parameter. Poor mixing of the Markov chains was also evident for the intercept and the shape parameter of the Weibull model. A possible way of overcoming this would have been to run further iterations; however, as this is not computationally efficient, a re-parameterised version of the Weibull model was adopted. This was combined with a parameter expansion technique to prevent the Gibbs sampler getting trapped near zero for the random effects. The re-parameterised version of the Weibull model reduced correlation in the Markov chains for the intercept and shape parameter; however, the parameter expansion did not have much effect at preventing the Gibbs sampler getting trapped near zero when fitted to the SHeS dataset.

Another problem with using a Bayesian approach was the time taken to estimate the models using MCMC. Even after adopting various techniques such as re-parameterisation and a parameter expansion technique to speed up convergence to reduce computing time, the time taken to estimate the models, especially those containing all significant covariates, was long. As the SHeS dataset was the smaller training dataset, it is envisaged that the same models fitted to an even

larger dataset could take a while to run. Unless computing time is not important, this approach could have the potential to be computationally inefficient for larger datasets.

9 Applying Alternative Methods to a Larger Dataset

9.1 Introduction

Methods which could potentially be used as an alternative to fitting multilevel continuous-time survival models were investigated and tested using the Scottish training dataset in previous chapters. As the Scottish dataset was moderately sized, in terms of the size of datasets used in public health, it is now of interest to establish how effective these potential alternative methods are when fitted to a much larger dataset.

9.2 Objectives using Swedish Data

The primary objective of the work on the Swedish dataset is to demonstrate how effective the alternative methods discussed in Chapter 7 are when fitted to a much larger dataset. However, the aim of the research is to investigate the association between sex, early-life socioeconomic conditions and either suicide or attempted suicide. A list of all available early-life socioeconomic risk factors was given in Table 2.2.

Recall that the Swedish dataset consists of two birth cohorts from the years 1972 and 1977. Therefore, it is also of interest to investigate how the background hazard in the outcome of interest, i.e. either an attempted suicide or death from suicide, varies between the two birth cohorts. Individuals were followed-up from the date of their 12th birthday, until either the event of interest occurred, or they died from a cause other than suicide, or the end of follow-up which was between 2003 and 2006. It is hypothesised that there may be differences between the two cohorts as a result of a period of recession during the 1990s in Sweden. Those in the older 1972 birth cohort would have been leaving high school and entering the labour market at the beginning of the recession period, whereas those in the younger 1977 cohort would have been leaving education

during the middle to late period of recession. It is thus expected that the background hazard of event may differ between the two cohorts depending on the time period.

9.3 Preliminary Analysis of Swedish Data

The Swedish dataset is hierarchical in nature, with 185963 individuals nested within 2596 parishes. These are, in turn, nested within 280 municipalities. It is clear that the Swedish dataset is much larger than the Scottish dataset, in terms of both the number of individuals and the number of years of follow-up. Details of the dataset were given in Section 2.3. Recall from Section 9.2 that interest was in investigating the effect of early-life socioeconomic conditions on attempted suicide and suicide following adjustment for cohort year.

This section gives an overview of the number of attempted suicides and suicides in the 1972 and 1977 cohorts. Some preliminary results for the objectives stated in Section 9.2, obtained from fitting multilevel logistic regression models, are given in Section 9.3.3.

9.3.1 Descriptive Statistics

Table 9.1 below displays the percentages of individuals who experienced the event of interest, i.e. either attempted or committed suicide, by cohort year.

Table 9.1 - Percentage of events by cohort year

	1972 Cohort	1977 Cohort	Total
Event			
Frequency	1971	1553	3524
Percent (%)	2.0	1.8	1.9
No Event			
Frequency	97487	84952	182439
Percent (%)	98.0	98.2	98.1
Total			
Frequency	99458	86505	185963
Percent (%)	100	100	100

Table 9.1 indicates that only a small percentage of individuals experienced the event of interest, which was either attempting or committing suicide (= 1.9%). This implies that, like the Scottish Health Survey dataset, there was a high percentage of censored observations in the Swedish dataset (= 98.2%). There was not much difference in the percentage of individuals attempting or committing suicide between the two cohorts (a difference of 0.2%). This is perhaps surprising since the 1972 cohort were followed up for a longer period of time and therefore, a greater percentage of events might have been expected amongst individuals belonging to this cohort.

Recall from Section 9.2, that one area of interest was to investigate how the recession in Sweden during the 1990s affected each of the two cohorts in terms of the number of attempted suicides or deaths from suicide. The plot in Figure 9.1 below can be used to form some informal impressions.

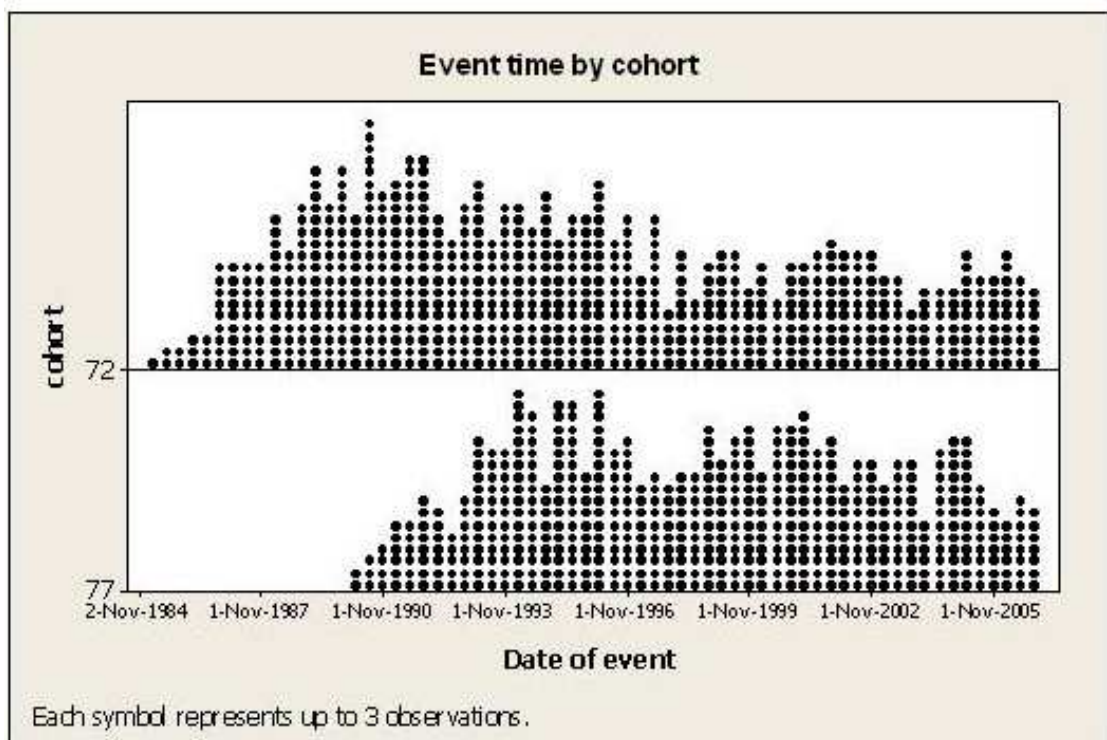


Figure 9.1 - Date of event by birth cohort year

From Figure 9.1 it can be observed that, in the 1972 cohort, the number of events gradually increased pre-1990s before the recession, i.e. between ages 12 and 18 years for this cohort. The highest number of events appeared to be during the recession (approximately 1992 - 1996/97), which was between ages

18 and 22 years, before declining in the post-recession period. Individuals in the 1977 cohort were around 13 years old when the recession began. There was a sharp rise in the number of events halfway through the period of recession (around 1993/94) for this cohort, i.e. around the ages 15 to 16 years. This would coincide with the age at which this cohort would be beginning to leave education to seek employment. The number of events peaked during the second half of the recession period (around 1995) towards 18 years old. This is around the time at which all individuals would have left secondary education. There was a slight decline in the number of events from the end of the recession period; however, it was not as marked as the decline in the 1972 cohort. This might suggest that the effects of the recession affected the younger cohort more; perhaps as they struggled to find employment on leaving education at the end of the recession period and thus leading to a greater number of attempted suicides or deaths from suicides.

Some information was also available on variables reflecting the early-life socioeconomic conditions of the individuals. Table 9.2 below displays the percentage of events by each early-life socioeconomic risk factor.

The following informal observations can be made from Table 9.2 in terms of the effect of early-life socioeconomic conditions on the percentage of events. A greater percentage of females than males experienced the event (difference of 0.9%); the percentage of events was highest for those whose fathers' social class was unclassifiable or missing (this category may have included unemployed persons as unclassifiable); there appeared to be an increasing trend in the percentage of events as the household income quintile at birth worsened, again with the highest percentage of events in the 'missing' category; a higher percentage of those in rented accommodation experienced the event than those in owner occupied accommodation (difference of 1.3%); and the percentage of events appeared highest among smaller regions, dominated by private enterprises.

Table 9.2 - Percentage of events by socioeconomic risk factors

	Attempted/Committed Suicide (%)
Sex	
Male	1.5
Female	2.4
Father's occupational social class (1980)	
Employers/Farmers/Entrepreneurs	1.6
Non-manual workers	1.3
Manual workers	2.0
Unclassifiable/Missing	3.5
Household income quintile at birth	
1 = lowest	2.2
2	1.8
3	1.7
4	1.8
5 = highest	1.3
Missing	4.2
Housing tenure at birth	
Owner occupied	1.5
Rented	2.8
Economic region	
Metropolitan areas	2.0
Larger regional centres	1.8
Smaller regional centres	1.7
Small regions (mostly private enterprises)	2.4
Small regions (mostly public sector)	2.0

Table 9.2 suggested that early-life socioeconomic conditions of children may have an effect on the likelihood of attempting or committing suicide as measured from age 12 years. It may also have been of interest to investigate whether the effect of these variables differed by age. This will be considered during formal analysis by fitting two-way interactions between cohort and each of the socioeconomic risk factors (and sex). Results from fitting these interactions will indicate whether the influence of early-life socioeconomic conditions on the likelihood of attempting or committing suicide varied between the different cohorts, i.e. the different ages.

9.3.2 Missing Data

There was missing data in the Swedish dataset for all explanatory variables apart from sex and birth cohort year. Due to the high percentage of missing data for the variables ‘father’s social class in 1980’ (14% missing), and ‘household income quintile at birth (4% missing)’, missing or unclassifiable observations for these variables were included as a separate category in analyses. It is perhaps sensible to include these as a separate category since it is possible that observations were classified as missing/unclassifiable as a result of unemployment. This will be considered further in Section 9.5.2. However, for the variable ‘housing tenure at birth’ only 0.3% had missing data and thus cases with data missing on this variable were excluded and not treated as a separate category. There was also missing data on the higher-level variable, ‘economic region’. Cases with missing data were excluded from analysis even though a high percentage of observations (12.3%) were coded as missing. No further information was available from the data source on why cases with missing data with this variable were excluded and not coded as a separate category.

Of the 185963 individuals in the Swedish dataset, 12.6% of individuals had missing data on at least one of the variables ‘economic region’ or ‘housing tenure at birth’. As discussed above, cases with missing data were excluded from analysis. This method of case deletion was adopted, as opposed to a method of imputation, due to time constraints on analyses. Consequences of ignoring missing data are discussed further in Chapter 10. After excluding cases with missing data on individual-level variables (housing tenure at birth) there were 185449 individuals, nested within 2596 parishes, nested within 280 municipalities. However, when excluding cases with missing data on all individual-level and higher-level variables (housing tenure at birth and economic region) there were only 162 539 individuals nested within 1988 parishes nested within 232 municipalities left for analyses.

9.3.3 Results from Preliminary Analyses of Swedish Data

This section presents results obtained from fitting single-level Cox proportional hazards models (PHM) in SPSS and multilevel logistic regression models in MLwiN. Results from the Cox PHM and multilevel logistic regression were fitted to gain an insight into expected results prior to fitting the more complex multilevel survival models. When fitting the single-level Cox PHM, the response was time until attempted suicide or death by suicide. Observations were censored if an individual died from any cause other than suicide or did not experience the event of interest during follow-up. Single-level models do not account for the fact that the data are hierarchically structured, consisting of three levels - individuals nested within parishes nested within municipalities. Instead, multilevel logistic regression models were fitted to investigate whether there were any differences in the likelihood of event across the higher levels. For the multilevel logistic regression, the binary response was of the form 'individual did or did not attempt or commit suicide', as measured from their 12th birthday. A binomial model with logit link was fitted in MLwiN, and the parameter estimates were obtained using second-order penalised quasi-likelihood (PQL) estimation. The outcome was assumed to be Binomially distributed.

Three models (using both a single-level Cox PHM and a multilevel logistic regression) were fitted to the data. The first contained individual-level variables only ('Individual'). The second model added higher-level variables to the model containing all individual variables ('Individual+Area') to see what percentage of the remaining variation at the higher-levels could be explained by these variables after adjustment for the individual-level variables. Finally, two-way interactions between all variables and cohort ('Full') were included to investigate whether the influence of early-life socioeconomic conditions on the likelihood of attempting or committing suicide varied by age. Results are displayed in Table 9.3 below. Note that the estimates obtained from the single-level Cox PHM are log hazard ratios and the estimates obtained from the multilevel logistic regression model are log odds ratios.

Table 9.3 - Results from preliminary analyses of Swedish data

	Single-Level Cox PHM			Multilevel Logistic Regression		
	Individual Estimate (s.e.)	Individual+Area Estimate (s.e.)	Full Estimate (s.e.)	Individual Estimate (s.e.)	Individual+Area Estimate (s.e.)	Full Estimate (s.e.)
Fixed						
Intercept (β_0)	-	-	-	-4.463 (0.070)	-4.416 (0.080)	-4.209 (0.099)
Sex						
<i>Male</i>	0.000**	0.000**	0.000**	0.000	0.000	0.000
<i>Female</i> (β_1)	0.475 (0.034)	0.496 (0.037)	0.452 (0.049)	0.481 (0.035)	0.502 (0.037)	0.458 (0.049)
Father Soc. Class 1980						
<i>Employers etc</i>	0.000**	0.000**	0.000**	0.000	0.000	0.000
<i>Non-manual</i> (β_2)	-0.107 (0.068)	-0.102 (0.073)	-0.174 (0.092)	-0.110 (0.069)	-0.104 (0.074)	-0.178 (0.093)
<i>Manual</i> (β_3)	0.168 (0.063)	0.169 (0.068)	0.137 (0.087)	0.166 (0.064)	0.167 (0.069)	0.135 (0.088)
<i>Unclassifiable</i> (β_4)	0.585 (0.068)	0.563 (0.073)	0.487 (0.092)	0.587 (0.069)	0.566 (0.074)	0.491 (0.094)
Hhold Income Quintile						
<i>Quintile 1</i>	0.000**	0.000**	0.000**	0.000	0.000	0.000
<i>Quintile 2</i> (β_5)	-0.132 (0.051)	-0.142 (0.055)	-0.234 (0.072)	-0.135 (0.052)	-0.145 (0.056)	-0.238 (0.073)
<i>Quintile 3</i> (β_6)	-0.164 (0.054)	-0.164 (0.057)	-0.269 (0.076)	-0.167 (0.055)	-0.166 (0.058)	-0.274 (0.077)
<i>Quintile 4</i> (β_7)	-0.090 (0.056)	-0.095 (0.059)	-0.228 (0.079)	-0.095 (0.057)	-0.098 (0.060)	-0.234 (0.081)
<i>Quintile 5</i> (β_8)	-0.246 (0.063)	-0.285 (0.067)	-0.401 (0.086)	-0.251 (0.064)	-0.288 (0.068)	-0.405 (0.088)
<i>Missing</i> (β_9)	0.490 (0.067)	0.463 (0.071)	0.397 (0.094)	0.500 (0.069)	0.473 (0.073)	0.406 (0.097)
Housing Tenure						
<i>Owner Occupied</i>	0.000**	0.000**	0.000**	0.000	0.000	0.000
<i>Rented</i> (β_{10})	0.478 (0.036)	0.484 (0.038)	0.454 (0.050)	0.475 (0.037)	0.484 (0.039)	0.453 (0.051)
Birth Cohort						
1972	0.000**	0.000**	0.000*	0.000	0.000	0.000
1977 (β_{11})	0.167 (0.036)	0.149 (0.038)	-0.326 (0.155)	-0.026 (0.035)	-0.039 (0.038)	-0.519 (0.157)

Economic Region					
<i>Metropolitan</i>	0.000*	0.000*		0.000	0.000
<i>Larger Regional</i> (β_{12})	-0.078 (0.041)	-0.104 (0.054)		-0.075 (0.044)	-0.101 (0.056)
<i>Smaller Regional</i> (β_{13})	-0.122 (0.058)	-0.278 (0.081)		-0.117 (0.062)	-0.274 (0.084)
<i>Private Enterprise</i> (β_{14})	0.148 (0.095)	0.188 (0.119)		0.147 (0.100)	0.189 (0.124)
<i>Public Sector</i> (β_{15})	-0.044 (0.129)	-0.230 (0.183)		-0.031 (0.135)	-0.221 (0.188)
Cohort*Sex		0.000			
<i>1972*Male</i>		0.102 (0.074)			0.000
<i>1977*Female</i> (β_{16})					0.102 (0.075)
Cohort*Soc. Class		0.000			
<i>1972*Employers etc</i>		0.164 (0.151)			0.000
<i>1977*Non-manual</i> (β_{17})		0.079 (0.142)			0.168 (0.153)
<i>1977*Manual</i> (β_{18})		0.181 (0.150)			0.080 (0.144)
<i>1977*Unclass.</i> (β_{19})					0.180 (0.152)
Cohort*Income		0.000			
<i>1972*Quintile 1</i>		0.209 (0.112)			0.000
<i>1977*Quintile 2</i> (β_{20})		0.240 (0.115)			0.212 (0.114)
<i>1977*Quintile 3</i> (β_{21})		0.299 (0.120)			0.246 (0.117)
<i>1977*Quintile 4</i> (β_{22})		0.276 (0.138)			0.305 (0.122)
<i>1977*Quintile 5</i> (β_{23})		0.147 (0.144)			0.280 (0.140)
<i>1977*Missing</i> (β_{24})					0.150 (0.148)
Cohort*Housing Tenure		0.000			
<i>1972*Owner Occupied</i>		0.078 (0.078)			0.000
<i>1977*Rented</i> (β_{25})					0.081 (0.080)
Cohort*Region		0.000*			
<i>1972*Metropolitan</i>		0.066 (0.082)			0.000
<i>1977*Larger reg.</i> (β_{26})		0.345 (0.117)			0.066 (0.084)
<i>1977*Smaller reg.</i> (β_{27})		-0.106 (0.196)			0.347 (0.119)
<i>1977*Private</i> (β_{28})		0.418 (0.258)			-0.109 (0.200)
<i>1977*Public</i> (β_{29})					0.423 (0.263)
Random					
Parish Variation(σ_u^2)			0.022 (0.012)	0.017 (0.011)	0.017 (0.011)
Municipal. Variation(σ_v^2)			0.000 (0.000)	0.000 (0.000)	0.000 (0.000)

From Table 9.3 it can be observed that, apart from the parameter estimates for birth cohort year, parameter estimates obtained from the single-level Cox PHM and the multilevel logistic regression were very similar. However, the parameter estimates obtained from the single-level Cox PH model and the multilevel logistic regression model for cohort year were not similar for the ‘Individual’ and ‘Individual+Area’ models. In the single-level model, there were significant differences in the hazard of event between the two cohorts after adjusting for other individual- and also other individual- and area-level variables. This effect was not present in the multilevel logistic regression model.

In the single-level Cox PHM with individual-level covariates only (‘Individual’), all of the covariates were found to have a highly significant effect on the hazard of attempting or committing suicide after adjusting for the others. Results showed the following, after adjusting for each of the other covariates: females had a significantly higher hazard of event than males; an increasing trend in the hazard of event was present as fathers’ social class became less professional/more manual, with those having fathers categorised as ‘unclassifiable or missing’ (which possibly includes unemployed persons) having the highest hazard of event; there was a general decreasing trend in the hazard of event as the household income at birth increased (i.e. the direction of the quintiles ranged 1 to 5), with the ‘missing’ category leading to the highest hazard of event (again, those classified as missing could be individuals whose parents were unemployed at the time of birth); those in rented accommodation at birth had a significantly higher hazard of event later in life than those in privately owned accommodation; and those in the 1977 cohort had a significantly higher hazard of event than those in the earlier 1972 cohort. When the higher-level variable ‘economic region’ was added to this model (‘Individual+Area’), the individual-level variables remained highly significant and parameter estimates did not change much. In addition to the individual-level variables, there was a significant effect of economic region on the hazard of attempting or committing suicide during follow-up. Finally, as discussed above, it was of interest to fit two-way interactions between all variables and cohort (‘Full’) to investigate whether the influence of early-life socioeconomic conditions on the likelihood of attempting or committing suicide differed between the two different cohorts. Results from the single-level PHM indicated

that the only significant interaction was between cohort year and economic region. Results suggest that the effect of economic region on the hazard of event was generally stronger for those born in 1977. This may coincide with the impression that the recession had a longer-lasting effect on the younger 1977 cohort. If such individuals were struggling to find employment post-recession, then it is possible that they were unable to move away from economic regions that could be having a damaging effect on their health.

As noted above, apart from the variable 'cohort', parameter estimates for the covariates in the 'Individual' and 'Individual+Area' models were similar when using the multilevel logistic regression model to when the single-level Cox PHM was used. However, as the data were hierarchical, with individuals nested within parishes nested within municipalities, it was more appropriate to use a multilevel model. This allowed the variation in the hazard of attempting or committing suicide to be partitioned into that attributable to differences between individuals and that attributable to differences between municipalities and parishes. In the 'Individual' multilevel logistic regression model, taking the antilogit function of the intercept indicated that, following adjustment for all individual-level covariates, the probability of attempting or committing suicide for a person with baseline characteristics in the average district within municipality was 0.011. There was no variation in the hazard of event at the highest level, i.e. between municipalities, and less than 1% (=0.66%) of the total variation was attributable to differences between parishes within municipalities. Adding economic region to the model (i.e. the 'Individual+ Area' model) explained 23% of the variation between parishes within municipalities. No further variation at the parish (within municipality) level was explained by adding two-way individual-level and cross-level interactions between each variable and cohort year. Parameter estimates for all two-way interactions obtained from the multilevel logistic regression model were similar to those obtained from the single-level Cox PHM. This suggests that the only significant two-way interaction was the cross-level interaction between birth cohort year and economic region.

9.3.4 Summary of Preliminary Analyses of Swedish Data

One objective of the Swedish dataset was to investigate the association between early-life socioeconomic conditions and the hazard of attempting or committing suicide, as measured from an individual's 12th birthday. Multilevel models must be used to account for the hierarchical nature of the data - individuals within parishes within municipalities.

Before fitting the more complex multilevel survival models, some preliminary analysis of the dataset, using single-level proportional hazards models and multilevel logistic regression models, was carried out in order to gain an insight into expected results. Results indicated that there were significant additive effects of sex and various measures of early-life socioeconomic conditions on the hazard or odds of event. There was also some evidence of a significant cross-level interaction between birth cohort year and economic region. The multilevel logistic regression model showed that there was no variation in the hazard of event at the municipality level, and less than 1% was attributable to differences between parishes within municipalities. It is expected that similar results will be observed when fitting multilevel survival models.

9.4 Fitting Multilevel Survival Models to the Swedish Dataset

As discussed in previous chapters, the proportional hazards model (PHM) is one of the most commonly used continuous-time models for modelling survival data. The single-level PHM may be extended to include random effects yielding a multilevel model. MLwiN is able to fit multilevel continuous-time proportional hazards models via a multilevel Poisson model fitted to a person-period dataset. As creation of the person-period dataset leads to an expansion in the size of the original dataset, computational problems can arise if the original dataset is large to begin with and/or if individuals are followed up for a long period of time. Thus, it is of interest to investigate alternative ways of fitting multilevel survival

models to large datasets since it is clear that continuous-time models can be problematic.

Previous chapters considered three possible alternatives to fitting continuous-time multilevel models in MLwiN. These included fitting discrete-time models in MLwiN, aggregating data according to covariates and fitting continuous- and discrete-time models to the aggregated data and fitting frailty models in WinBUGS. The three methods were fitted to a moderately-sized Scottish dataset in order to test their suitability as an alternative to the continuous-time models fitted in MLwiN. This section will now consider whether the alternative methods are still appropriate when fitted to a much larger Swedish dataset. The dataset is large in terms of the number of individuals and the period of follow-up.

9.4.1 Multilevel Continuous-Time Survival Models

It was of interest to investigate whether MLwiN would be able to estimate a continuous-time proportional hazards model, fitted via a Poisson model, to the large Swedish dataset. First, the person-period dataset had to be created. The ‘SURV’ command in MLwiN is used to perform the data expansion. However, the Swedish dataset proved to be much too large to use the ‘SURV’ command in order to create the expanded dataset when time was treated as a continuous variable, i.e. measured in days. As the person-period dataset could not be created, multilevel PH models, fitted via Poisson models in MLwiN, could not be implemented in this package. Recall also that, due to the high percentage of censored observations in the Swedish dataset (98%), the accelerated lifetime (log-duration) model, which does not require any data expansion, could not be used. This is because of the tendency of the quasi-likelihood estimation procedure to break down for this model in the presence of many censored observations. Furthermore, as there were three hierarchical levels in the Swedish data, the only other readily available statistical package that could be used to fit multilevel survival models is WinBUGS (refer to Section 5.3.2). Fitting multilevel survival (frailty) models in WinBUGS is considered in Section 9.4.4.

9.4.2 Multilevel Discrete-time Survival Models

Multilevel discrete-time models (fitted in MLwiN) were found to be a useful alternative to fitting continuous-time models in MLwiN when tested on the moderately-sized Scottish Health Survey dataset. Time was divided into short intervals, of either equal or varying length, leading to a reduction in the number of risk sets and hence a reduction in the size of the expanded person-period dataset. Discrete-time models were easily implemented using multilevel logistic regression models fitted to the person-period dataset. It was of interest to see how well these models would perform when fitted to a much larger dataset.

Various groupings were considered when dividing up time to form the discrete-time intervals. It was of interest to investigate the largest number of discrete-time intervals that MLwiN would allow before the person-period dataset became too large and estimating the models became problematic. Conversely, it was also of interest to determine the smallest number of discrete-time intervals permitted without losing precision by having wide intervals.

Table 9.4 below summarises the various attempts at dividing up time. It displays whether time was divided into intervals of equal or varied lengths according to when each event occurred, how many risk sets resulted from the division and the size of the expanded dataset for each particular division. Finally, it indicates whether each of the three models described in Section 9.3.3, i.e. the ‘Individual’, ‘Individual+Area’ and ‘Full’ models, as well as a baseline model containing no covariates, could be estimated in MLwiN. Information on the estimation procedure used is also displayed. Parameter estimates for the three models fitted to the smallest and largest datasets resulting from the various groupings are then displayed in Table 9.7. Checks of proportionality assumptions are included in Appendix 6.

Table 9.4 shows that grouping time into year-long intervals led to an expanded dataset that was too large to allow the estimation of models. The expanded dataset for this particular grouping of time consisted of 3801822 observations within individuals - twice as many as the moderately sized Scottish Health Survey dataset which consisted of approximately 1.9 million observations within individuals in the continuous-time case. Further grouping of time into intervals

of length 2 years halved the size of the expanded dataset from when time was grouped in years; however, estimation of models was still problematic and only the baseline model, with no covariates, included could be estimated.

There were four alternative groupings for intervals of varied length considered in Table 9.4. The groupings were defined according to days when clusters of events occurred when looking at dotplots of the event/survival times. Groupings for the expanded dataset with 3 risk sets are given in Table 9.5 and in Table 9.6 for the expanded dataset with 7 risk sets. Groupings for the other expanded datasets can be found in Appendix 5. It can be observed that, as the number of risk sets decreased, i.e. the lengths of the intervals became longer, the size of the expanded dataset also decreased.

Table 9.4 - Dividing time in the Swedish dataset

Division	No. of Risk Sets	Size of Expanded Dataset	Baseline	Individual	Individual+Area	Full
Equal year-long intervals	23	3 801 822	-	-	-	-
Equal two-year long intervals	12	1 950 471	Polynomial PQL2			
Varied - defined by events	10	1 668 284	Blocking Factors PQL2	PQL2	PQL2	-
Varied - defined by events	7	1 202 560	Blocking Factors PQL2	PQL2	PQL2	PQL2
Varied - defined by events	5	921 279	Blocking Factors PQL2	PQL2	PQL2	PQL2
Varied - defined by events	3	553 652	Blocking Factors PQL2	PQL2	PQL2	PQL2

Table 9.5 - Discrete-time grouping for expanded dataset with 3 risk sets

Time Interval	Grouping
1	Day 0 – day 2700
2	Day 2701 – day 4500
3	Day 4501 – day 8373
4	Day 8374 – day 8500

Table 9.6 - Discrete-time grouping for expanded dataset with 7 risk sets

Time Interval	Grouping
1	Day 0 – day 1700
2	Day 1701 – day 2700
3	Day 2701 – day 3500
4	Day 3501 – day 4500
5	Day 4501 – day 5900
6	Day 5901 – day 6900
7	Day 6901 – day 8373
8	Day 8374 – day 8500

Table 9.5 displays the division of time for the expanded dataset with 3 risk sets. Note that, although there were 4 distinct time intervals, the last time interval contains only censored observations (since the last event occurred at 8373 days from 12th birthday), and therefore was not included as a risk set since no events occurred during that interval. Note that the last event for those in the 1977 cohort was 6502 days from 12th birthday. Similarly, for the expanded dataset with 7 risk sets (Table 9.6), there were 8 distinct time intervals; however, the last time interval contained censored observations only and thus was not included as a risk set.

Table 9.7 - Results from fitting multilevel discrete-time models to Swedish data

	Varied Intervals with 3 Risk Sets			Varied Intervals with 7 Risk Sets		
	Individual Estimate (s.e.)	Individual+Area Estimate (s.e.)	Full Estimate (s.e.)	Individual Estimate (s.e.)	Individual+Area Estimate (s.e.)	Full Estimate (s.e.)
Fixed						
Intercept (β_0)	-5.509 (0.073)	-5.472 (0.083)	-5.267 (0.102)	-6.450 (0.081)	-6.412 (0.090)	-6.207 (0.108)
Time2 (α_1)	-0.138 (0.042)	-0.117 (0.045)	-0.117 (0.045)	0.349 (0.058)	0.351 (0.062)	0.351 (0.062)
Time3 (α_2)	-0.032 (0.041)	-0.024 (0.044)	-0.024 (0.044)	-0.096 (0.064)	-0.099 (0.069)	-0.099 (0.069)
Time4 (α_3)	-	-	-	0.180 (0.060)	0.222 (0.064)	0.222 (0.064)
Time5 (α_4)	-	-	-	0.235 (0.059)	0.254 (0.063)	0.254 (0.063)
Time6 (α_5)	-	-	-	-0.490 (0.072)	-0.492 (0.077)	-0.492 (0.077)
Time7 (α_6)	-	-	-	-0.132 (0.081)	-0.145 (0.087)	-0.145 (0.087)
Sex						
Male	0.000	0.000	0.000	0.000	0.000	0.000
Female (β_1)	0.478 (0.035)	0.499 (0.037)	0.455 (0.049)	0.477 (0.035)	0.498 (0.037)	0.454 (0.049)
Father Soc. Class 1980						
Employers etc	0.000	0.000	0.000	0.000	0.000	0.000
Non-manual (β_2)	-0.110 (0.068)	-0.104 (0.073)	-0.177 (0.093)	-0.109 (0.068)	-0.104 (0.073)	-0.177 (0.092)
Manual (β_3)	0.165 (0.064)	0.166 (0.069)	0.134 (0.087)	0.165 (0.064)	0.165 (0.069)	0.134 (0.087)
Unclassifiable (β_4)	0.581 (0.068)	0.560 (0.073)	0.485 (0.093)	0.579 (0.068)	0.559 (0.073)	0.484 (0.093)
Hhold Income Quintile						
Quintile 1	0.000	0.000	0.000	0.000	0.000	0.000
Quintile 2 (β_5)	-0.134 (0.052)	-0.144 (0.056)	-0.236 (0.073)	-0.133 (0.052)	-0.144 (0.056)	-0.235 (0.073)
Quintile 3 (β_6)	-0.166 (0.054)	-0.165 (0.058)	-0.271 (0.076)	-0.166 (0.054)	-0.165 (0.057)	-0.271 (0.076)
Quintile 4 (β_7)	-0.094 (0.056)	-0.097 (0.060)	-0.231 (0.080)	-0.094 (0.056)	-0.097 (0.060)	-0.231 (0.080)
Quintile 5 (β_8)	-0.250 (0.064)	-0.286 (0.068)	-0.402 (0.087)	-0.250 (0.064)	-0.286 (0.068)	-0.402 (0.087)
Missing (β_9)	0.493 (0.068)	0.466 (0.072)	0.399 (0.095)	0.491 (0.068)	0.464 (0.072)	0.397 (0.095)
Housing Tenure						
Owner Occupied	0.000	0.000	0.000	0.000	0.000	0.000
Rented (β_{10})	0.472 (0.037)	0.481 (0.039)	0.449 (0.051)	0.470 (0.037)	0.479 (0.039)	0.448 (0.051)

Birth Cohort						
1972	0.000	0.000	0.000	0.000	0.000	0.000
1977 (β_{11})	-0.025 (0.035)	-0.038 (0.037)	-0.514 (0.156)	0.103 (0.036)	0.087 (0.038)	-0.389 (0.156)
Economic Region						
Metropolitan		0.000	0.000		0.000	0.000
Larger Regional (β_{12})		-0.074 (0.043)	-0.100 (0.056)		-0.074 (0.043)	-0.100 (0.056)
Smaller Regional (β_{13})		-0.116 (0.061)	-0.271 (0.083)		-0.116 (0.061)	-0.270 (0.083)
Private Enterprise(β_{14})		0.147 (0.099)	0.189 (0.123)		0.147 (0.098)	0.189 (0.123)
Public Sector (β_{15})		-0.032 (0.133)	-0.219 (0.187)		-0.032 (0.133)	-0.218 (0.187)
Cohort*Sex						
1972*Male			0.000			0.000
1977*Female (β_{16})			0.102 (0.075)			0.102 (0.074)
Cohort*Soc. Class						
1972*Employers etc			0.000			0.000
1977*Non-manual (β_{17})			0.166 (0.152)			0.166 (0.152)
1977*Manual (β_{18})			0.080 (0.143)			0.080 (0.142)
1977*Unclass. (β_{19})			0.180 (0.151)			0.179 (0.151)
Cohort*Income						
1972*Quintile 1			0.000			0.000
1977*Quintile 2 (β_{20})			0.210 (0.113)			0.210 (0.113)
1977*Quintile 3 (β_{21})			0.242 (0.116)			0.242 (0.116)
1977*Quintile 4 (β_{22})			0.301 (0.121)			0.301 (0.120)
1977*Quintile 5 (β_{23})			0.277 (0.139)			0.277 (0.139)
1977*Missing (β_{24})			0.150 (0.146)			0.150 (0.145)
Cohort*Housing Tenure						
1972*Owner Occupied			0.000			0.000
1977*Rented (β_{25})			0.080 (0.079)			0.080 (0.079)
Cohort*Region						
1972*Metropolitan			0.000			0.000
1977*Larger reg. (β_{26})			0.064 (0.083)			0.064 (0.083)
1977*Smaller reg. (β_{27})			0.344 (0.118)			0.343 (0.117)
1977*Private (β_{28})			-0.108 (0.198)			-0.108 (0.197)
1977*Public (β_{29})			0.418 (0.261)			0.417 (0.260)

Random						
Parish Variation(σ_u^2)	0.022 (0.011)	0.017 (0.011)	0.017 (0.011)	0.022 (0.011)	0.017 (0.011)	0.017 (0.011)
Municipal. Variation(σ_v^2)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)

Table 9.7 displays results obtained from fitting the three models ('Individual', 'Individual+Area' and 'Full') to the expanded dataset with 3 risk sets and the expanded dataset with 7 risk sets. It was discussed above that it was of interest to compare parameter estimates from the models fitted to the smallest and largest expanded datasets resulting from the various groupings of time. This was in order to determine whether precision had been lost by having a fewer number of longer time intervals. The fewer the number of time intervals, the smaller the size of the expanded dataset, meaning that models can be estimated in a shorter time. The person-period dataset with 7 risk sets was chosen to compare results from the person-period dataset with 3 risk sets. This was because it was the largest expanded dataset that allowed estimation of all three models (see Table 9.4). Blocking factors were used to estimate the baseline hazard function in these models. A polynomial function could also have been used for the expanded dataset with 7 risk sets of varied lengths to reduce the number of nuisance parameters to be estimated.

The first aspect to be considered from Table 9.7 was whether the three models, fitted to both of the different sizes of expanded dataset, yielded similar parameter estimates. Considering just the 'Individual' and 'Individual+Area' models, it was observed that the parameter estimates for all covariates, apart from 'cohort', were very similar for the two different datasets. However, in the 'Individual' and 'Individual+Area' models fitted to the expanded dataset with 3 risk sets, there was no significant effect of cohort on the hazard of attempting or committing suicide following adjustment for the other covariates. This was not the case for the same models fitted to the expanded dataset with 7 risk sets. In this case, there was a significant effect of cohort, with those born in 1977 having a significantly higher hazard of event during follow-up than those born in 1972, after adjusting for the other covariates. This suggested that, when time was divided into intervals of longer length, the effect of cohort on the hazard of event was being lost. This will be considered below.

The estimates of the alpha parameters in the models indicated the change in the baseline hazard as time increased, i.e. as individuals get older. The baseline hazard was fitted using blocking factors, i.e. dummy variables, where the baseline hazard of event in each risk set was compared to the baseline hazard in the first risk set. The intercept, β_0 , denotes the hazard of event in the first risk

set. For the models fitted to the expanded dataset with 3 risk sets, the parameter estimates for alpha indicated that there was a significantly lower hazard of event during the second risk set compared to the first risk set, i.e. a lower hazard of event when individuals were aged 19-24 years than when they were aged 12-19 years. There were no significant differences in the baseline hazard between the third and first risk set, i.e. between ages 24-34 years (24-29 years for those in the 1977 cohort) and 12-19 years. This was not what was observed from the models fitted to the expanded dataset with 7 risk sets. Instead it can be seen that, compared to the first risk set, i.e. aged 12-16 years, there was a significantly higher hazard of event in the second risk set (aged 16-19 years), the fourth risk set (aged 21-24 years) and the fifth risk set (aged 24-28 years). In addition, there was a significantly lower hazard of event in the sixth risk set (age 28-30 for 1972 cohort and 28-29 for the 1977 cohort) than in the first risk set. These differences were not observed when the broader groupings of time were used, i.e. when there were only 3 risk sets.

There was no clear evidence of any two-way interactions between cohort year and the socioeconomic variables in the 'Full' models fitted to the expanded dataset with 3 or with 7 risk sets.

Parameter estimates from the multilevel discrete-time survival models were compared to those obtained from the single-level PHM and the multilevel logistic regression. Parameter estimates for the 'Individual', 'Individual+Area' and the 'Full' models fitted using the three different methods (single-level PHM, multilevel logistic and multilevel survival) were similar for all parameters apart from 'cohort'. Parameter estimates for 'cohort' obtained from the single-level PH models were similar to those obtained from the multilevel discrete-time models fitted to the expanded dataset with 7 risk sets. However, parameter estimates obtained for this variable from the multilevel logistic regression models were more similar to those obtained from the multilevel discrete-time model fitted to the expanded dataset with 3 risk sets. This demonstrated again that the parameter estimate for 'cohort' was affected by the way time was divided. This result is not unexpected since it is known that parameter estimates of coefficients depend on the length of the time interval when the logistic model is used to fit the discrete-time hazard model [156, 157]. Allison [156] and Petersen [157] gave a detailed overview of this problem and discussed that, if

the width of the time interval is small (and hence the probability of an event in each time interval is small), then the logistic model converges to the proportional hazards model, and coefficients obtained from using a discrete-time model will be quite similar to those obtained from a continuous-time model. Also, if the probability of event is small, only the intercept term depends on the length of the time interval, with changes in the time unit tending to have no influence on the other coefficients. Petersen and Allison offered some possible solutions to overcome the problem of the dependence of coefficients on the length of time intervals. Petersen discussed an estimator which could be used to adjust for time aggregation bias. Alternatively, both Allison & Petersen discussed that a complementary log-log link function could be used instead of the logistic regression function. They discussed how the complementary log-log model is unaffected by the length of time intervals, and would provide consistent estimators of the continuous-time proportional hazards model, regardless of the length of time intervals.

With the knowledge that parameter estimates for the regression parameters can be affected by the length of time interval, it is somewhat interesting that only the coefficients for the variable 'cohort' (after accounting for the other variables in the model) seemed to be affected by having a smaller number of risk sets of longer length. This indicates that the effect of cohort on the hazard of event depended on the length of time interval used, suggesting an interaction between time and cohort. With this in mind, the next step in analysis would be to include a two-way interaction between time and cohort to investigate whether the effect of time on the hazard of event differs by cohort. It seemed reasonable to assume that the parameter estimates obtained from the models fitted to the expanded dataset with 7 risk sets were more accurate than those obtained from the models fitted to the expanded dataset with 3 risk sets. This view was held since the former obtained estimates which were more similar to those produced by the single-level proportional hazards model, where time was treated as a continuous variable. It should be noted also that the same three models were fitted to an expanded dataset containing 5 risk sets (results displayed in Appendix 7); however, the estimates of cohort in each of the models were more similar to those obtained from the models fitted to the expanded dataset with 3 risk sets, thus suggesting that the groupings of time

used in this case were still too large to provide consistent estimators of the proportional hazards parameters.

From fitting three different models to the expanded datasets, i.e. 'Individual', 'Individual+Area' and 'Full', it was observed that the 'Individual+Area' model, which included all individual- and higher-level additive effects, was the most appropriate model. This was because it explained the largest amount of variation in the hazard of event at the higher level, and also because there were no significant two-way interactions between cohort year and any of the other socioeconomic variables. Therefore, a two-way interaction between time and cohort was included in the 'Individual+Area' model fitted to the expanded dataset with 7 risk sets. Results are displayed in Table 9.8 below.

Results from Table 9.8 for the two-way interaction between time and cohort indicated that, after adjusting for early-life socioeconomic risk factors, the hazard of attempting or committing suicide in the third risk set (i.e. aged 19-21) and in the sixth risk set (i.e. aged 28-30 for those in the 1972 cohort and 28-29 for those in the 1977 cohort) compared to the first risk set was significantly lower for those in the 1977 cohort than those in the 1972 cohort. This difference could reflect the effect of the recession on the hazard of event; those in the 1972 cohort would have been trying to find employment in the middle of the recession when aged 19-21 years, whereas the recession had passed by the time those in the 1977 cohort were aged 19-21 years and were perhaps seeking employment. The difference in the hazard of event during the 6th risk set between the two cohorts possibly just reflected the end of follow-up for those in the 1977 cohort, thus censoring any remaining individuals. As expected, the parameter estimate for the time*cohort interaction in the seventh risk set (i.e. B_{22}) was zero, simply indicating the longer period of follow-up for those in the 1972 cohort. Finally, parameter estimates and estimated standard errors for all additive effects remained unchanged as a result of adding the interaction between time and cohort. Addition of this term did not explain any more of the variation in the hazard of event at the parish level.

Table 9.8 - Results from investigating the effect of cohort

	Estimate (s.e.)	
Fixed		
Intercept (β_0)	-6.506	(0.101)
Time 1	0.000	
Time2 (α_1)	0.468	(0.086)
Time3 (α_2)	0.055	(0.095)
Time4 (α_3)	0.298	(0.090)
Time5 (α_4)	0.179	(0.092)
Time6 (α_5)	-0.091	(0.099)
Time7 (α_6)	-0.052	(0.098)
Sex		
Male	0.000	
Female (β_1)	0.498	(0.037)
Father Soc. Class 1980		
Employers etc	0.000	
Non-manual (β_2)	-0.104	(0.073)
Manual (β_3)	0.165	(0.069)
Unclassifiable (β_4)	0.559	(0.073)
Hhold Income Quintile		
Quintile 1	0.000	
Quintile 2 (β_5)	-0.144	(0.056)
Quintile 3 (β_6)	-0.165	(0.057)
Quintile 4 (β_7)	-0.097	(0.060)
Quintile 5 (β_8)	-0.286	(0.068)
Missing (β_9)	0.464	(0.072)
Housing Tenure		
Owner Occupied	0.000	
Rented (β_{10})	0.479	(0.039)
Birth Cohort		
1972	0.000	
1977 (β_{11})	0.278	(0.095)
Economic Region		
Metropolitan	0.000	
Larger Regional (β_{12})	-0.074	(0.043)
Smaller Regional (β_{13})	-0.116	(0.061)
Private Enterprise(β_{14})	0.147	(0.098)
Public Sector (β_{15})	-0.032	(0.133)
Time*Cohort		
1972*Time 1 (β_{16})	0.000	
1977*Time 2 (β_{17})	-0.244	(0.124)
1977*Time 3 (β_{18})	-0.326	(0.138)
1977*Time 4 (β_{19})	-0.154	(0.127)
1977*Time 5 (β_{20})	0.141	(0.127)
1977*Time 6 (β_{21})	-1.032	(0.166)
1977*Time 7 (β_{22})	0.000	(0.000)
Random		
Parish Variation(σ_u^2)	0.017	(0.011)
Municipal. Variation(σ_v^2)	0.000	(0.000)

9.4.3 Grouping According to Covariates

If individuals nested within the same higher-level units have the same values for covariates included in a particular model, then it is clear that these individuals are at risk of experiencing the event of interest at the same time. The data for these individuals can be aggregated so that only one line of data represents all such individuals, thus leading to a reduction in the size of the expanded person-period dataset. This so-called ‘grouping according to covariates’ method was found to successfully reduce the size of the expanded Scottish Health Survey dataset, especially when time was treated as a discrete variable. It was therefore of interest to investigate if this method performed as well when fitted to the much larger Swedish dataset.

There were a number of points to consider before applying this method to the Swedish dataset. Firstly, since the data aggregation must be carried out using the expanded dataset, time could only be treated as a discrete variable since the Swedish dataset was much too large to expand in MLwiN when time was being treated as continuous. Secondly, in the Scottish dataset, individuals were nested within postcode-sectors only, but in the Swedish dataset, there is a further higher level, with individuals being nested within parishes, which are in turn nested within municipalities. However, as parishes are nested within municipalities, the grouping will be the same as it would be if municipalities were ignored.

To apply this method to the Swedish dataset, the expanded dataset with 7 risk sets was used for aggregation. Four models were fitted to the expanded dataset after aggregation; the ‘Individual’ model, the ‘Individual+Area’ model, the ‘Full’ model and the ‘Individual+Area’ model which also included a two-way interaction between time and cohort. To fit these models, two aggregated datasets had to be created. The first aggregated data for individuals in the same parish and municipality with the same values for individual-level covariates and the second aggregated data for individuals within the same parish and municipality with the same values for individual-level and higher-level covariates. Although time was discrete, Poisson models were used for reasons discussed in Section 8.2.2, and the logarithm of the cell size was used as the

offset. Blocking factors were used to model the baseline hazard function. All models were estimated using second-order PQL. Table 9.9 displays the percentage reduction in the expanded dataset with 7 risk sets after aggregation. Recall, from Table 9.4, that the size of the expanded dataset with 7 risk sets was 1 202 560. Results are displayed in Table 9.10 below, and parameter estimates should be compared to those in Tables 9.7 and 9.8.

Table 9.9 - Percentage reduction in expanded dataset when grouping according to covariates

Covariate Grouping	Size of New Dataset	% Reduction
Individual	531 726	56%
Individual+Area	531 726	56%

Table 9.9 shows that when data for individuals nested in the same parish within municipality were aggregated according to values of individual-level covariates, the reduction in size from the expanded dataset with 7 risk sets was 56%.

Sections 8.2.3 and 8.4 discussed how the percentage reduction would decrease as the number of covariates to be grouped on increased; however, it can be seen from Table 9.9 that this was not the case when a further higher-level covariate was added to the list of covariates to be grouped on. The higher-level variable that was added, economic region, indicates what type of area the parish within municipality is; therefore, it is expected that all individuals in the same parish within municipality would have the same categorical value for this variable. As a result, it was not surprising that adding this variable to the list of covariates to be grouped on had no effect on the percentage reduction.

Table 9.10 - Results from grouping according to covariates with Swedish data

	Varied Intervals with 7 Risk Sets			
	Individual Estimate (s.e.)	Individual+Area Estimate (s.e.)	Full Estimate (s.e.)	Individual+Area+Time*Cohort Estimate (s.e.)
Fixed				
Intercept (β_0)	-6.452 (0.080)	-6.415 (0.090)	-6.209 (0.108)	-6.508 (0.101)
Time2 (α_1)	0.348 (0.058)	0.349 (0.062)	0.349 (0.062)	0.466 (0.086)
Time3 (α_2)	-0.095 (0.064)	-0.098 (0.069)	-0.098 (0.069)	0.055 (0.094)
Time4 (α_3)	0.180 (0.060)	0.221 (0.063)	0.221 (0.063)	0.296 (0.089)
Time5 (α_4)	0.235 (0.059)	0.253 (0.063)	0.253 (0.063)	0.178 (0.092)
Time6 (α_5)	-0.488 (0.072)	-0.490 (0.077)	-0.490 (0.077)	-0.090 (0.098)
Time7 (α_6)	-0.131 (0.081)	-0.144 (0.086)	-0.144 (0.086)	-0.052 (0.097)
Sex				
Male	0.000	0.000	0.000	0.000
Female (β_1)	0.474 (0.035)	0.494 (0.037)	0.452 (0.049)	0.494 (0.037)
Father Soc. Class 1980				
Employers etc	0.000	0.000	0.000	0.000
Non-manual (β_2)	-0.106 (0.068)	-0.100 (0.073)	-0.176 (0.092)	-0.100 (0.073)
Manual (β_3)	0.168 (0.064)	0.169 (0.069)	0.134 (0.087)	0.169 (0.069)
Unclassifiable (β_4)	0.581 (0.068)	0.561 (0.073)	0.482 (0.093)	0.561 (0.073)
Hhold Income Quintile				
Quintile 1	0.000	0.000	0.000	0.000
Quintile 2 (β_5)	-0.134 (0.052)	-0.144 (0.055)	-0.234 (0.072)	-0.144 (0.055)
Quintile 3 (β_6)	-0.165 (0.054)	-0.164 (0.057)	-0.269 (0.076)	-0.164 (0.057)
Quintile 4 (β_7)	-0.093 (0.056)	-0.097 (0.059)	-0.229 (0.080)	-0.097 (0.059)
Quintile 5 (β_8)	-0.249 (0.064)	-0.285 (0.068)	-0.400 (0.087)	-0.285 (0.068)
Missing (β_9)	0.490 (0.067)	0.464 (0.071)	0.394 (0.095)	0.464 (0.071)
Housing Tenure				
Owner Occupied	0.000	0.000	0.000	0.000
Rented (β_{10})	0.468 (0.037)	0.477 (0.039)	0.447 (0.051)	0.477 (0.039)

Birth Cohort				
1972	0.000	0.000	0.000	0.000
1977 (β_{11})	0.102 (0.036)	0.086 (0.038)	-0.395 (0.156)	0.276 (0.095)
Economic Region				
Metropolitan		0.000	0.000	0.000
Larger Regional (β_{12})		-0.074 (0.043)	-0.099 (0.056)	-0.074 (0.043)
Smaller Regional (β_{13})		-0.115 (0.061)	-0.270 (0.083)	-0.115 (0.061)
Private Enterprise (β_{14})		0.147 (0.098)	0.188 (0.122)	0.147 (0.098)
Public Sector (β_{15})		-0.032 (0.133)	-0.218 (0.186)	-0.032 (0.133)
Cohort*Sex				
1972*Male			0.000	
1977*Female (β_{16})			0.098 (0.074)	
Cohort*Soc. Class				
1972*Employers etc			0.000	
1977*Non-manual (β_{17})			0.176 (0.152)	
1977*Manual (β_{18})			0.091 (0.143)	
1977*Unclass. (β_{19})			0.192 (0.151)	
Cohort*Income				
1972*Quintile 1			0.000	
1977*Quintile 2 (β_{20})			0.204 (0.112)	
1977*Quintile 3 (β_{21})			0.239 (0.116)	
1977*Quintile 4 (β_{22})			0.298 (0.120)	
1977*Quintile 5 (β_{23})			0.275 (0.139)	
1977*Missing (β_{24})			0.154 (0.144)	
Cohort*Housing Tenure				
1972*Owner Occupied			0.000	
1977*Rented (β_{25})			0.077 (0.079)	
Cohort*Region				
1972*Metropolitan			0.000	
1977*Larger reg. (β_{26})			0.064 (0.083)	
1977*Smaller reg. (β_{27})			0.342 (0.117)	
1977*Private (β_{28})			-0.107 (0.197)	
1977*Public (β_{29})			0.416 (0.259)	

Time*Cohort				
1972*Time 1 (β_{30})				0.000
1977*Time 2 (β_{31})				-0.242 (0.123)
1977*Time 3 (β_{32})				-0.324 (0.138)
1977*Time 4 (β_{33})				-0.152 (0.127)
1977*Time 5 (β_{34})				0.141 (0.126)
1977*Time 6 (β_{35})				-1.029 (0.166)
1977*Time 7 (β_{36})				0.000 (0.000)
Random				
Parish Variation(σ_u^2)	0.021 (0.011)	0.016 (0.011)	0.016 (0.011)	0.016 (0.011)
Municipal. Variation(σ_v^2)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)

From examining parameter estimates for the ‘Individual’ model in Table 9.10 and comparing them to results obtained from fitting the same model before aggregation of the dataset with 7 risk sets (Table 9.7), it can be seen that parameter estimates and estimated standard errors, of both the fixed and random effects, were either identical or very similar following data aggregation to what they were prior to aggregating the data. This was also true of the ‘Individual+Area’ model. When two-way interactions between birth cohort year and the socioeconomic risk factors (and sex) were added to the model fitted to the aggregated dataset with 7 risk sets (i.e. the ‘Full’ model), parameter estimates for the interaction terms were not as similar to those obtained from the same model fitted to the dataset with 7 risk sets before aggregation as they had been for the main effects. However, the differences were not especially large, and 95% confidence intervals (not displayed here) for the parameter estimates of the interaction terms in the model fitted to the aggregated dataset contained the estimates of the respective parameters obtained from fitting the same model to the same dataset before aggregation. Finally, when comparing results from the ‘Individual+Area+Time*Cohort’ model (Table 9.10), it can be seen that parameter estimates and estimated standard errors of all fixed effects and random effects were either identical or very similar to those obtained for the same model fitted to the same dataset before aggregation (results in Table 9.8). Recall that, this model included all socioeconomic risk factors (and sex) and a two-way interaction between birth cohort year and the dummy variables for time (used to estimate the baseline hazard function).

This section has shown that the grouping according to covariates method has performed well, even on a larger dataset with a longer period of follow-up time, as compared to the Scottish ‘training’ dataset. This method can be deemed successful for the Swedish dataset since aggregating the person-period dataset led to a high percentage reduction (56%) in the size of the same dataset before aggregation. More importantly, however, parameter estimates were either identical or very similar to those obtained before aggregation. A possible explanation as to why this method has been successful for this dataset may be the large number of individuals living within each parish. After deletion of all individuals with missing data, there were approximately 82 individuals per parish on average. As discussed in Section 8.4, for a higher level unit consisting of a

larger number of individuals, there is a greater chance that more of these individuals will share the same values for the covariates to be grouped on. This could be why the percentage reduction in the expanded dataset with 7 risk sets following aggregation was so large at over a fifty percent reduction.

9.4.4 Bayesian Frailty Models

As discussed throughout this thesis, fitting multilevel proportional hazards models in MLwiN, whether they are continuous-time models or discrete-time (proportional odds) models, requires the creation of a person-period dataset. This inevitably leads to an expansion in the size of the original dataset. One alternative to fitting multilevel survival models in MLwiN, as reviewed in Section 7.4, is to adopt a Bayesian approach. Although the Poisson model used to estimate the proportional hazards model in MLwiN can be fitted using a Bayesian approach, MCMC methods used to estimate the Bayesian model can result in long computing times. Instead, the so-called ‘shared frailty’ model can be used, where the frailty term, equal to the exponential of the random effects, $w_j = \exp(u_j)$, accounts for the clustering of individuals within higher-level units. WinBUGS can be used to fit the shared-frailty model. An additive frailty model is adopted by WinBUGS and a Weibull distribution is assumed for the survivor function (refer to Section 7.4.4). Using this method does not require any data expansion. This section will present results obtained from fitting the shared frailty model in WinBUGS to the Swedish dataset.

Many distributions can be assumed for the frailty parameter (details in Section 7.4.3.1); however, as when fitting this model to the Scottish dataset in Chapter 8, a log-Normal distribution was adopted for this term. Additionally, prior distributions also had to be specified for all unknown parameters in the model. As in Chapter 8, vague Normal priors were assumed for the regression parameters, and the shape parameter of the Weibull distribution was assigned a log-Normal distribution. Finally, a vague Uniform hyperprior was assumed for the random-effects standard deviation. Results from fitting the additive frailty model including all individual- and higher-level additive effects (i.e. the ‘Individual+Area’ model) and the same model also including a two-way

interaction between the baseline hazard function, ‘time’, and birth cohort year (i.e. the Individual+Area+Time*Cohort model) are presented in Table 9.11. Trace plots and Gelman-Rubin plots are presented in Figures 9.2 and 9.3 respectively. Only plots for the intercept, α , shape parameter, r , higher-level variance, σ_u^2 , and regression parameters for one of the covariates (for cohort), β_{11} , are displayed. Plots for all other regression parameters can be found in Appendix 8. Table 9.12 displays the Monte Carlo error (MC error) as a percentage of the standard deviation for each parameter. Recall from Section 7.4.6.3 that this method is used to assess the accuracy of the posterior estimates. Spiegelhalter et al. [245] recommended that the simulations should be run until the MC error for each parameter of interest is less than around 5% of the sample standard deviation.

Recall from Section 8.3.2 that the beta regression parameters may be interpreted as hazard ratios. Note that only the two models discussed above were fitted since it was shown that the additive model including covariates from all levels explained the largest amount of variation at the higher-level. Also, the effect of time on the hazard of event seemed to differ between cohorts, suggesting that the two-way interaction between those terms should be included in the model. As it was anticipated that the frailty models fitted to the Swedish data using MCMC estimation would take a few days to run, information on municipality has been discarded in order to reduce computing time. This information could be discarded since previous results have shown that there was no variation in the hazard of event at this level. Thus, a two-level model has been fitted, with individuals nested within parishes. The results obtained from this model may be compared to those obtained from using the discrete-time model (Tables 9.7 and 9.8) and the grouping according to covariates approach (Table 9.10).

	Individual+Area Estimate (s.e.)	Individual+Area+Time* Cohort Estimate (s.e.)
Fixed		
Intercept (α)	-14.16 (0.388)	-14.64 (0.374)
Sex		
<i>Male</i>	0.000	0.000
<i>Female</i> (β_1)	0.496 (0.035)	0.493 (0.037)
Father Soc. Class 1980		
<i>Employers etc</i>	0.000	0.000
<i>Non-manual</i> (β_2)	-0.106 (0.064)	-0.096 (0.077)
<i>Manual</i> (β_3)	0.167 (0.060)	0.172 (0.070)
<i>Unclassifiable</i> (β_4)	0.558 (0.066)	0.566 (0.074)
Hhold Income Quintile		
<i>Quintile 1</i>	0.000	0.000
<i>Quintile 2</i> (β_5)	-0.142 (0.054)	-0.140 (0.055)
<i>Quintile 3</i> (β_6)	-0.161 (0.060)	-0.159 (0.059)
<i>Quintile 4</i> (β_7)	-0.094 (0.060)	-0.089 (0.057)
<i>Quintile 5</i> (β_8)	-0.281 (0.071)	-0.285 (0.069)
<i>Missing</i> (β_9)	0.460 (0.071)	0.466 (0.071)
Housing Tenure		
<i>Owner Occupied</i>	0.000	0.000
<i>Rented</i> (β_{10})	0.477 (0.039)	0.483 (0.037)
Birth Cohort		
1972	0.000	0.000
1977 (β_{11})	0.229 (0.039)	-0.052 (0.211)
Economic Region		
<i>Metropolitan</i>	0.000	0.000
<i>Larger Regional</i> (β_{12})	-0.074 (0.043)	-0.068 (0.043)
<i>Smaller Regional</i> (β_{13})	-0.117 (0.059)	-0.111 (0.059)
<i>Private Enterprise</i> (β_{14})	0.144 (0.093)	0.153 (0.098)
<i>Public Sector</i> (β_{15})	-0.032 (0.135)	-0.033 (0.133)
Shape		
r	1.081 (0.043)	
r ₁ (cohort1972)		1.132 (0.040)
r ₂ (cohort1977)		1.166 (0.048)
Random		
Parish Variation(σ_u^2)	0.015 (0.010)	0.015 (0.012)

Table 9.11 - Results from fitting Bayesian frailty models to Swedish data

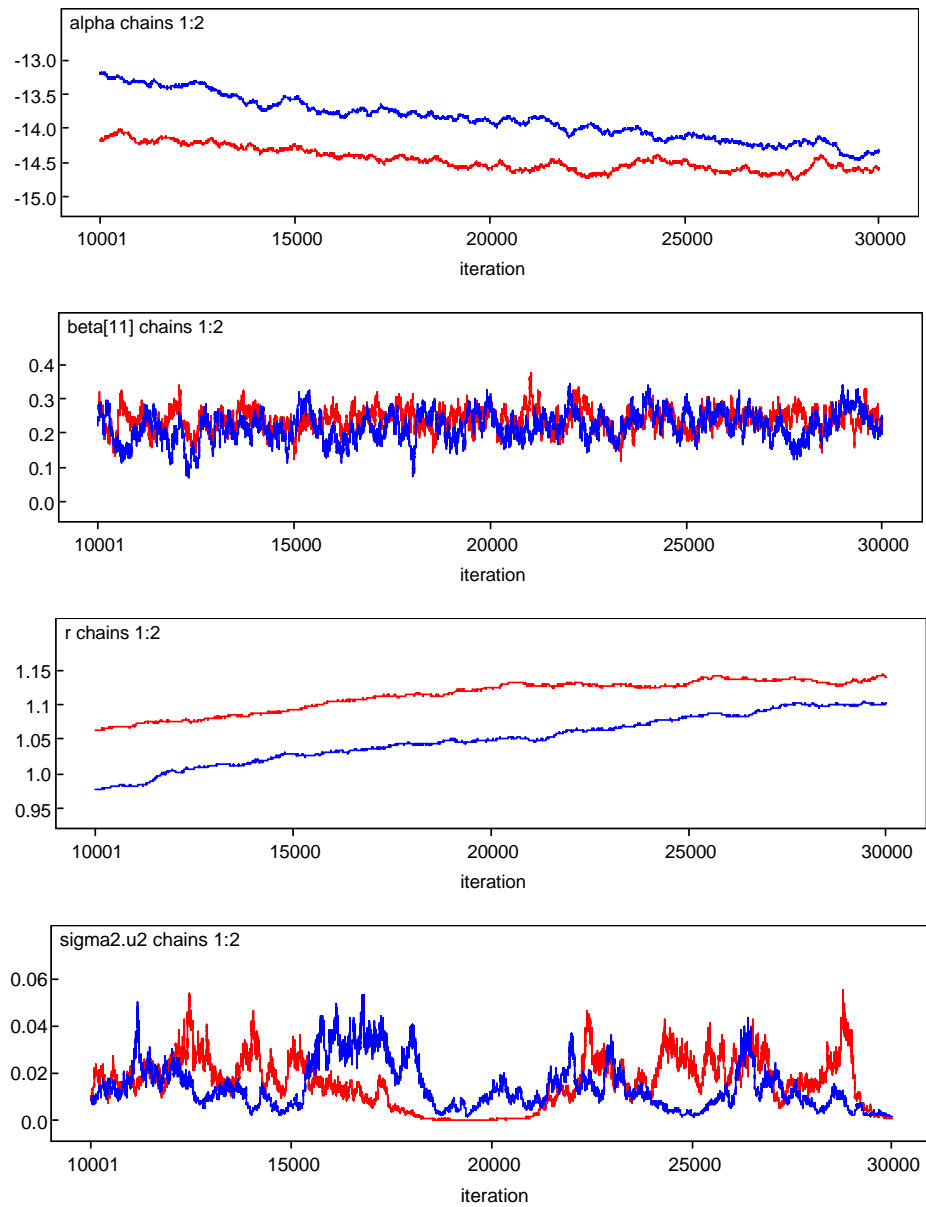


Figure 9.2 - Trace plots for 'Individual+Area' Model

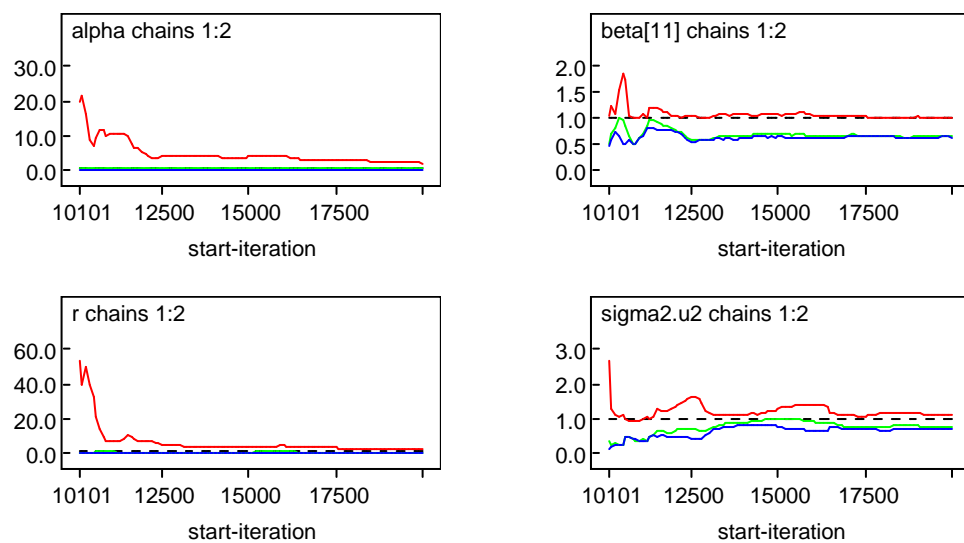


Figure 9.3 - Gelman-Rubin plots for 'Individual+Area' model

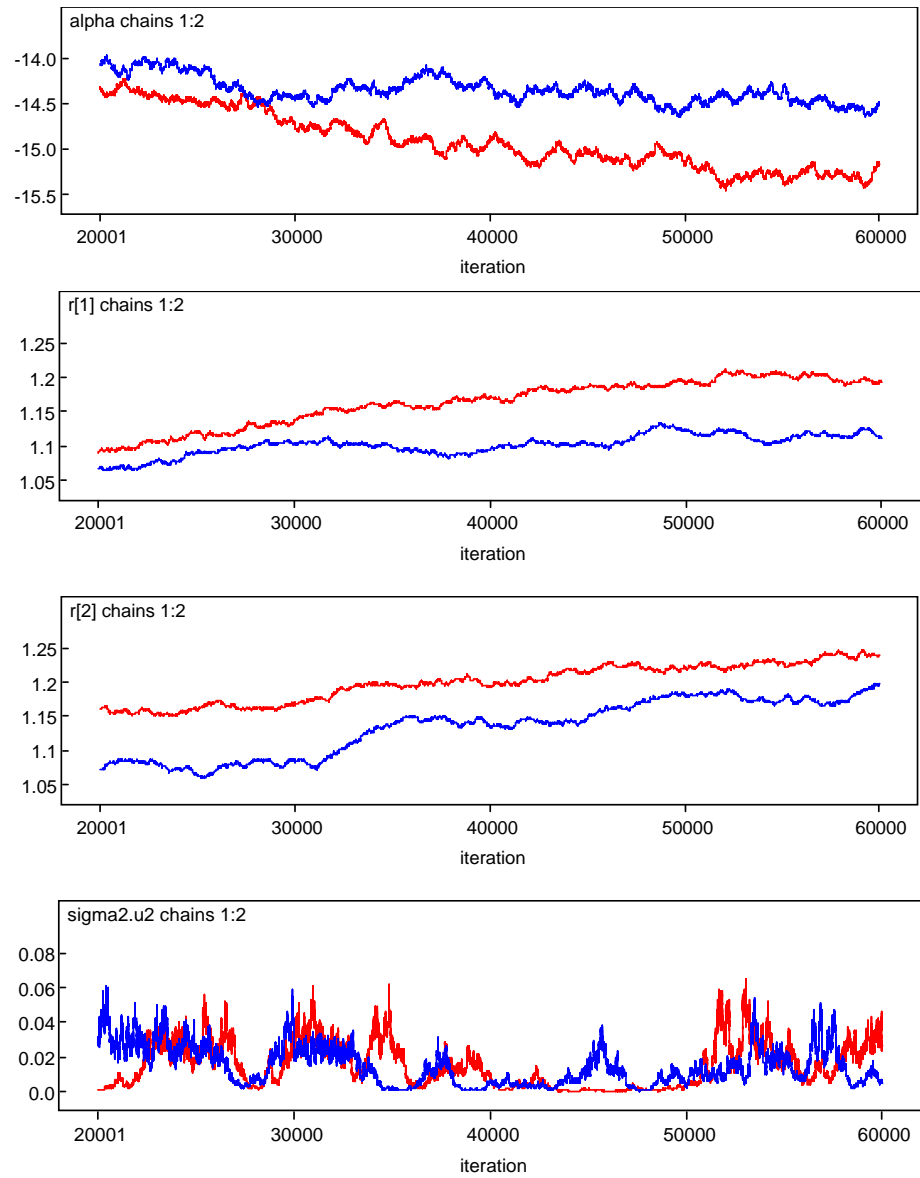


Figure 9.4 - Trace plots for 'Individual+Area+Time*Cohort' Model

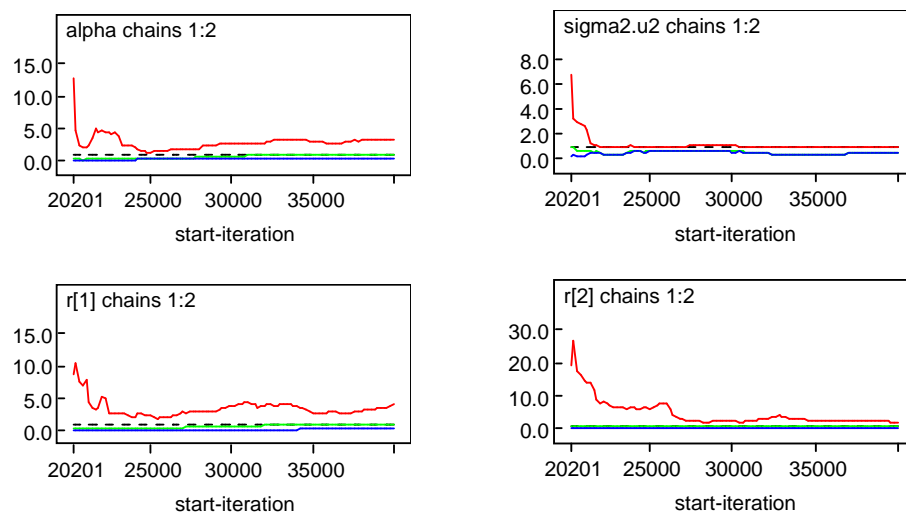


Figure 9.5 - Gelman-Rubin plots for 'Individual+Area+Time*Cohort' Model

Table 9.12 - MC error as a percentage of posterior standard deviation

	Individual+Area	Individual+Area+Time*Cohort
	MCE as % of SD	MCE as % of SD
α	6.0	5.0
β_1	4.8	3.8
β_2	5.5	4.6
β_3	5.4	4.6
β_4	5.2	4.3
β_5	4.9	4.0
β_6	5.0	4.0
β_7	4.9	3.9
β_8	5.3	4.1
β_9	4.1	3.1
β_{10}	4.7	3.5
β_{11}	5.0	5.0
β_{12}	4.9	3.9
β_{13}	4.6	3.5
β_{14}	4.1	3.1
β_{15}	4.2	3.2
r	6.0	
r_1 (cohort1972)		5.0
r_2 (cohort1977)		5.0
σ_u^2	5.7	4.8

For a burn-in period of 10000 iterations followed by a further 20000 iterations, CPU time for the ‘Individual+Area’ frailty model was 251 064s; however, in real time it was approximately 3.5 days. From comparing parameter estimates for this model in Table 9.11 to those presented in Tables 9.7 and 9.10, obtained using the discrete-time models and grouping according to covariates method respectively, it can be seen that parameter estimates and standard errors for the higher-level variation and all regression parameters apart from ‘cohort’ were very similar. However, the parameter estimate for ‘cohort’ obtained from fitting the Bayesian frailty model ($=0.229$) was larger than when discrete-time models were fitted to the dataset before aggregation ($=0.087$) and after aggregation according to covariates ($=0.086$). There are a few possible reasons that could explain this difference. Firstly, from observing the trace plot in Figure 9.2 for this parameter (β_{11}), it can be seen that a bigger burn-in period might have been required as the chains were not mixing perfectly by the end of the allotted burn-in period (10000 iterations). The Gelman-Rubin plot for this same parameter (Figure 9.3) indicated that a burn-in period of 12500 iterations may have been

preferred. Furthermore, Table 9.12 indicated that running a greater number of iterations after attaining convergence would have improved the accuracy of the posterior estimate. However, Table 9.12 indicated that this was also the case for most of the other model parameters. Although running further iterations may have improved the accuracy of the posterior estimates for all parameters, parameter estimates for all apart from 'cohort' using the frailty model were nevertheless found to be very similar to those obtained using the other methods described in Sections 9.4.2 and 9.4.3. Therefore, it is questionable as to whether running more iterations would have changed the estimate of the parameter for 'cohort' enough to be more similar to the estimates obtained using the other methods.

Another possible explanation is that the lengths of the intervals being used to fit the discrete-time models were too wide, even when the smaller grouping to form 7 risk sets as opposed to only 3 risk sets was used. This was discussed in Section 9.4.2 when comparing results from fitting discrete-time models using the two different groupings of time. This section noted that parameter estimates of coefficients are dependent on the length of time interval used. Since the frailty model treats time as continuous, it may therefore seem appropriate to assume that the estimate of 'cohort' obtained from this model is most likely to be correct. When comparing this estimate to the single-level proportional hazards model (Table 9.3), where time was also treated as continuous, it can be seen that there were still some differences between the estimates; however, the parameter estimate obtained from the single-level PHM ($=0.149$) only narrowly missed being included in the 95% credible interval (not displayed here).

The estimate of the shape parameter ($=1.081$) suggested that it was plausible that the hazard rate of event following adjustment for all individual- and higher-level covariates was strictly increasing in a non-linear pattern as time increased; however, the 95% credible interval (not displayed) included 1, indicating that it was, in fact, plausible that the hazard rate remained constant as time increased.

Other points arising from fitting the 'Individual+Area' frailty model included poor mixing of the chains for the intercept and shape parameters. This was evident from the trace plots for both displayed in Figure 9.2. There was also an apparent correlation between the chains for these two parameters. This had

been a cause for concern when fitting the frailty model to the Scottish dataset. Section 8.3.4 considered a re-parameterised version of the Weibull model which could be fitted as a possible way of eliminating this correlation. Finally, the trace plot for the higher-level variance in Figure 9.2 indicated that the Gibbs sampler was tending to get trapped near zero. This resulted in slow convergence for the parameter. This was another problem to have been observed when fitting the frailty model to the Scottish dataset. A parameter expansion technique aiming to speed up convergence was suggested in Section 8.3.5. The re-parameterised Weibull model with variance expansion of Section 8.3.5 was fitted to the Swedish dataset. Results are displayed in Table 9.13. Note that, due to time constraints, this technique was only considered for the model containing additive effects only (i.e. without the two-way interaction between ‘time’ and ‘cohort’). Trace plots and Gelman-Rubin plots for the intercept, shape parameter of the Weibull distribution, higher-level variance and the regression parameters for ‘cohort’ are given in Figures 9.6 and 9.7 respectively. Note that plots for other regression parameters in the model are not displayed here.

To fit a two-way interaction between ‘time’ and ‘cohort’, the shape parameter of the Weibull distribution was defined separately for each cohort. This allowed the hazard to assume different shapes for each birth cohort year. The WinBUGS code used to fit this model is given in Appendix 9. The model was run for a burn-in period of 20000 iterations followed by a further 40000 iterations. CPU time was 486 183 seconds. Parameter estimates for this model were compared with those in Tables 9.7 and 9.10 for the same model. It can be observed that estimates of all main effects (excluding ‘cohort’) and the higher level variance were similar across the three tables (Tables 9.7, 9.10 and 9.11). The estimates of the main effects and higher-level variance for the ‘Individual+Area’ and ‘Individual+Area+Time*Cohort’ obtained from fitting the Weibull model (Table 9.11) can also be compared. Table 9.12 indicated that the posterior estimates for the ‘Individual+Area+Time*Cohort’ were more accurate than the ‘Individual+Area’ model, as the Monte Carlo error (MCE) for each parameter was 5% or less of the sample standard deviation. This was not the case for all parameters in the ‘Individual+Area’ model. The improvements in the accuracy of the results were most likely a consequence of running a further number of iterations following the burn-in period.

The trace plots for the regression parameters (excluding 'cohort') in Figure 9.4 indicated that the burn-in period of 20000 iterations was sufficient for attaining convergence since the multiple chains in each plot were mixing well and were stable around the mean value. However, it can also be observed that the multiple chains for the intercept and shape parameters were not mixing well, and there was evidence of correlation in the chains for these two parameters. Furthermore, the trace plot for the higher-level variance indicated that the Gibbs sampler was prone to getting trapped near zero. The re-parameterised Weibull model with variance expansion may have been required to resolve these problems.

Of most interest, however, are the estimates of the shape parameters defined for each birth cohort year. Results in Table 9.11 indicated that the hazard function for those in the 1977 cohort ($r_2 = 1.166$) is increasing more steeply than for those in the 1972 birth cohort ($r_1 = 1.132$), thus confirming an interaction between 'time' and birth cohort year. It should be noted, however, that there is quite a lot of overlap in the 95% credible intervals (not displayed here) for r_1 and r_2 .

Table 9.13 - Results from fitting re-parameterised Weibull model with variance expansion to the Swedish dataset

	Individual+Area Estimate (s.e.)
Fixed	
Intercept (α)	-15.44 (0.225)
Sex	
<i>Male</i>	0.000
<i>Female</i> (β_1)	0.490 (0.034)
Father Soc. Class 1980	
<i>Employers etc</i>	0.000
<i>Non-manual</i> (β_2)	-0.132 (0.072)
<i>Manual</i> (β_3)	0.133 (0.067)
<i>Unclassifiable</i> (β_4)	0.527 (0.073)
Hhold Income Quintile	
<i>Quintile 1</i>	0.000
<i>Quintile 2</i> (β_5)	-0.150 (0.056)
<i>Quintile 3</i> (β_6)	-0.176 (0.059)
<i>Quintile 4</i> (β_7)	-0.112 (0.065)
<i>Quintile 5</i> (β_8)	-0.299 (0.067)
<i>Missing</i> (β_9)	0.451 (0.070)
Housing Tenure	
<i>Owner Occupied</i>	0.000
<i>Rented</i> (β_{10})	0.480 (0.040)
Birth Cohort	
1972	0.000
1977 (β_{11})	0.267 (0.035)
Economic Region	
<i>Metropolitan</i>	0.000
<i>Larger Regional</i> (β_{12})	-0.082 (0.043)
<i>Smaller Regional</i> (β_{13})	-0.124 (0.060)
<i>Private Enterprise</i> (β_{14})	0.142 (0.095)
<i>Public Sector</i> (β_{15})	-0.045 (0.136)
Shape (r)	1.228 (0.026)
Random	
Parish Variation(σ_u^2)	0.012 (0.010)

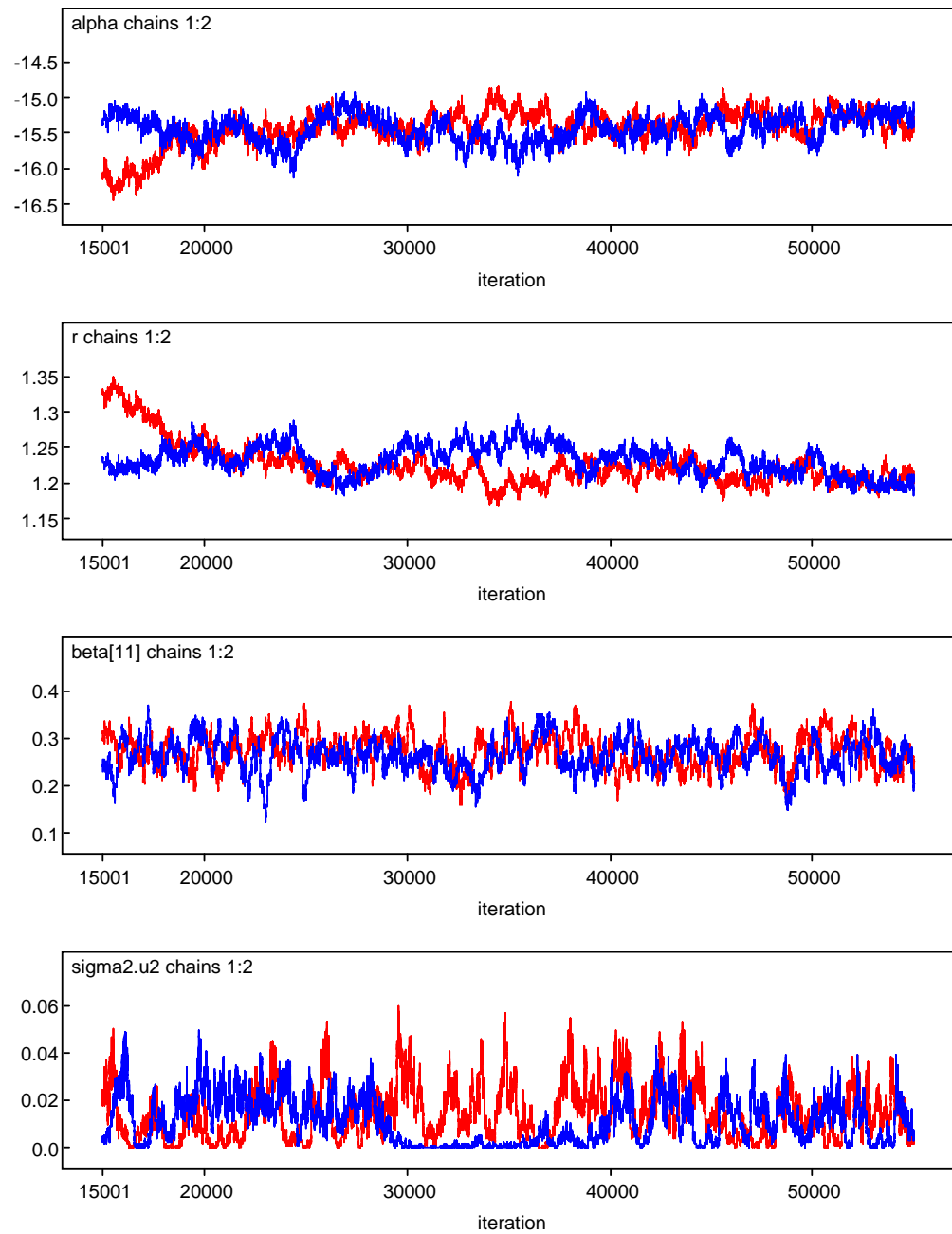


Figure 9.6 - Trace plots for re-parameterised Weibull model with variance expansion

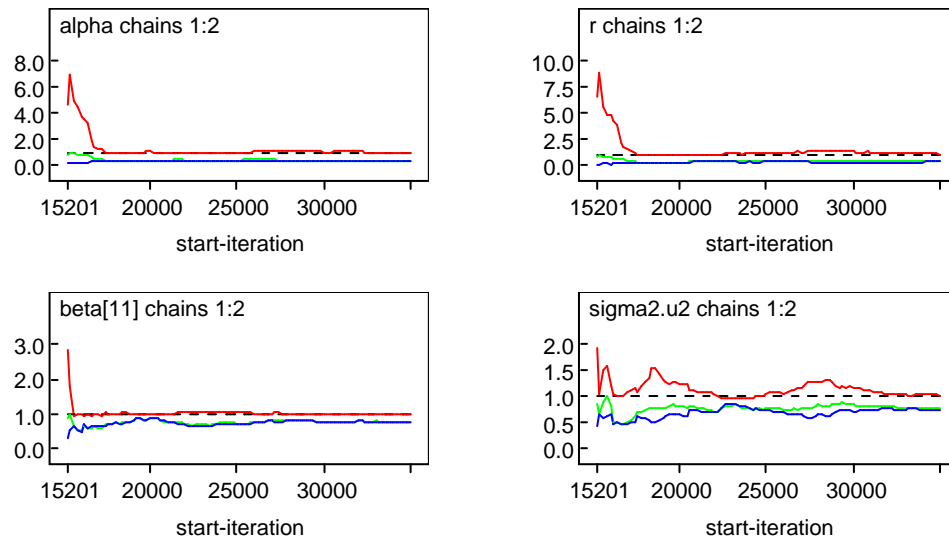


Figure 9.7 - Gelman-Rubin plots for re-parameterised Weibull model with variance expansion

The re-parameterised Weibull model with parameter expansion was run for a burn-in period of 15000 iterations, with a further 40000 iterations run after the burn-in period to obtain posterior estimates. CPU time was 593 835 seconds, i.e. approximately seven days. Recall that this model was fitted in order to try and eliminate the correlation between the chains for the intercept, alpha and the shape parameter, r . Therefore, parameter estimates, trace plots and Gelman-Rubin plots should be compared to Table 9.11 and Figures 9.2 and 9.3 respectively.

To determine whether using a re-parameterised version of the Weibull model has eliminated the correlation between the intercept and the shape parameter, it was of most interest to observe the trace plots for these parameters (Figure 9.6) and compare them to the trace plots for the same parameters in Figure 9.2. It can be seen that the multiple chains for both the intercept and the shape parameter were mixing better in Figure 9.6 following the re-parameterisation than in Figure 9.2. There was still some evidence of correlation in the multiple chains; however, it had been greatly reduced following the re-parameterisation. This would support the use of the re-parameterised model.

It was also of most interest to compare the trace plot for the higher-level variance, σ_u^2 , in Figure 9.6 to that in Figure 9.2 in order to determine whether using a parameter expansion technique had been successful in preventing the

Gibbs sampler getting trapped near zero. From comparing the trace plots, it can be observed that the multiple chains for this parameter were mixing much better and were not as prone to getting trapped near zero following the use of the parameter expansion (Figure 9.6). The Gelman-Rubin plot for this parameter in Figure 9.7 suggested that a bigger burn-in period may have been required, perhaps around 25000 to 30000 iterations. However, regardless of this, the variance expansion appeared to have successfully improved convergence for the higher-level variance by preventing the Gibbs sampler from getting stuck near zero.

It was also of interest to compare parameter estimates in Table 9.13 to those in Table 9.11. It can be observed that the parameter estimate of the intercept was reduced following the re-parameterisation (-15.44 compared to -14.16). The standard deviation was also smaller indicating better precision in the estimate following the re-parameterisation. The estimate of the shape parameter had increased slightly following the re-parameterisation (1.228 compared to 1.081) and, unlike the 95% credible interval (not displayed here) for this parameter before the re-parameterisation (Table 9.11), the 95% credible interval following the re-parameterisation did not include 1, and indicated that it was plausible that the hazard rate was increasing as time increased. Using the variance expansion technique did not alter the estimates of the higher-level variance when comparing results in Table 9.13 to those in Table 9.11. Similarly, estimates of the regression parameters seemed similar and in the cases where there were slight differences, 95% credible intervals (not displayed here) for the re-parameterised Weibull model with variance expansion contained the values of the estimates obtained using the original Weibull model (Table 9.11).

9.5 Conclusions: Results from the Swedish Data

The Swedish dataset consisted of 185963 individuals from two birth cohort years, 1972 and 1977. All individuals were followed up from the date of their 12th birthday until at least 2003, with a final end date for follow-up in 2006. From this it is clear that the length of follow-up differs between the two cohorts, with

those in 1972 being followed up for a longer period of time. The dataset was hierarchical in nature, with the 185963 individuals nested within 2596 parishes, which were in turn nested within 280 municipalities. Primary interest with this dataset was to investigate the effect of early-life socioeconomic conditions on attempted suicide and suicide, following adjustment for birth cohort year. It was anticipated, that, because of a period of recession in Sweden during the 1990s, there could be differences in the likelihood of an individual experiencing the event of interest depending on their year of birth. Individuals in the older 1972 cohort would have been finishing education and seeking employment during the recession, whereas individuals in the younger 1977 cohort would have been finishing their education and seeking employment nearer the end of the recession period. The outcome was time until either the first attempted suicide or death from suicide. Observations were censored if the individual did not attempt or commit suicide by the end of the follow-up period, or if they died from causes other than suicide. The main findings will be summarised in this section, with a further discussion on limitations of the dataset, and the suitability of each of the alternative methods when applied to the larger dataset.

9.5.1 Summary of Findings from the Swedish Dataset

The first model to be fitted to the Swedish dataset included all individual-level early-life socioeconomic risk factors only (as well as gender). Results from this model (using all methods for fitting multilevel survival models) indicated that there was a significant difference in the hazard of event between the two birth cohorts after adjusting for all other variables. Those in the younger 1977 cohort had a significantly higher hazard of event than those in the 1972 cohort. In addition to being born in 1977, other significant risk factors for a greater hazard of event included the following: being female, having a father with social class categorised as either 'manual' or 'missing' in 1980, the household income at birth being categorised as 'missing' and living in rented accommodation at birth. After adjusting for all significant risk factors, the probability of attempting or committing suicide for a person with baseline characteristics in the average

parish within municipality was small (≈ 0.00158). All variation was at parish level (i.e. there was no variation in the hazard of event between municipalities), and was bordering on significance. Although the between-parish variation was fairly small (≈ 0.022), it was large in comparison to the hazard of event in the average parish within municipality.

A contextual-level variable was then added to the model containing all individual-level variables. This variable was an indicator of the type of economic region. Although there were no significant differences when comparing each level of region to the baseline, i.e. metropolitan regions, adding this variable to the model explained some more of the variation between parishes within municipalities ($\approx 23\%$ of the variation). Whilst the effect of cohort on the hazard of event was attenuated when adding economic region, there were still significant differences between the two cohorts after adjusting for the other variables.

Two further models were fitted; one which included all individual- and higher-level additive effects plus two-way interactions between cohort and each of the other variables and another which included all additive effects and a two-way interaction between time and cohort. It was of interest to fit the first model to investigate if the effect of gender and each of the early-life socioeconomic risk factors on the hazard of event differed between the two birth cohort years. Generally, there was no strong indication that the effect of gender and the socioeconomic variables on the hazard of event differed between cohort years; however, there was a suggestion that living in smaller regional centres (compared to metropolitan areas) significantly increased the hazard of event for those born in 1977 compared to those born in 1972. There was also a weak suggestion that the hazard of event was significantly higher for those born in 1977 compared to those born in 1972 when household income at birth was in the third or fourth quintile (compared to quintile 1).

Finally, results from the model containing all additive effects plus a two-way interaction between time and cohort suggested that as time increased, the hazard of attempting or committing suicide differed between the two cohorts. It could be observed that the hazard of event in the third and sixth risk sets (compared to the first risk set) differed between the two cohorts, with those in

the 1977 cohort having a significantly higher hazard of event at these times than those in the 1972 cohort. An explanation of this result was given in Section 9.4.2.

9.5.2 Limitations of the Data

The main limitation of the Swedish dataset was the lack of information available on reasons for missing data. Results showed that those categorised as ‘unclassifiable or missing’ for the variables ‘father’s social class in 1980’ and ‘household income at birth’ had the highest hazard of event compared to the baseline categories. It would have been beneficial to know why these data had been coded as ‘unclassifiable or missing’ in the first place, in order to determine what it was about those categories that increased the hazard of event. One possible explanation could have been unemployment. If an individual’s father was unemployed in 1980 then it may not have been possible to assign one of the other social class categories to this observation. Similarly, if there was no household income at birth, then observations may again just have been coded as missing. If this were the case, then it would suggest that individuals whose parents were unemployed during early childhood years could be at greater risk of attempting or committing suicide during their teenage years and in early adulthood.

Another point concerning missing data was the way it was handled during analyses. Although individuals with missing data for the ‘social class’ and ‘household income’ variables were coded as a separate category and included in analysis as described above, some individuals also had missing data for the ‘housing tenure at birth’ and ‘economic region’ variables. Individuals with missing data on either of these variables were excluded from analysis. As discussed in Section 4.1.3, ignoring missing data can lead to loss of power or biased estimates of associations. Since it is known that even a small proportion of missing data can potentially bias results, it would have been preferable to impute values for the missing data rather than exclude the cases; however, due to time constraints on analyses, methods of missing value imputation were not employed. This would be a recommendation for further work with this dataset.

9.6 Conclusions: Suitability of Methods

The primary aim of using the Swedish dataset was to investigate which of the alternative methods described in Chapter 7 performed well when fitted to a much larger dataset. The Swedish dataset was larger than the Scottish ‘training’ dataset, in terms of both the number of individuals and the length of follow-up. As with the Scottish dataset, there was a high percentage of censored observations in the Swedish dataset (approximately 98%). This section summarises how well each of the methods being considered as an alternative to fitting multilevel continuous-time proportional hazards models in MLwiN performed when fitted to the large Swedish dataset.

Since the Swedish dataset was large to begin with (containing 185 963 individuals), it was anticipated that treating time as a continuous variable would not be a plausible option. As discussed throughout this thesis, fitting multilevel continuous-time models in MLwiN requires the creation of a person-period dataset so that each individual’s record is replicated for each time point until the individual experiences the event of interest or is censored. When an event is rare, this implies that most individuals will have a line of data for all time points, which poses a problem if the period of follow-up is long. The Swedish dataset was much too large to allow creation of the person-period dataset in MLwiN when time was being treated as a continuous variable (i.e. measured in days). Thus, alternative methods had to be adopted in order to fit multilevel survival models to this dataset.

The first alternative method to be considered involved defining different risk sets, so that time was divided into discrete intervals instead of being treated as continuous. Various groupings of time were considered for the Swedish dataset, as displayed in Table 9.4. It was of interest to investigate how narrow intervals could be before estimating models in MLwiN became problematic. Recall that the shorter the length of the time interval the more risk sets there are, thus resulting in a larger person-period dataset. Similarly, it was also of interest to determine the smallest number of risk sets permitted without losing precision in the estimates by having long time intervals. The smallest person-period dataset which could successfully fit multilevel discrete-time survival models in MLwiN

without losing precision in estimates contained just over 1.2 million observations within individuals. Results from fitting multilevel discrete-time models were presented and discussed in Section 9.4.2. Results suggested that various groupings of time should be considered when defining discrete time intervals in order to ensure that no information is being lost by having wider intervals and thus, fewer risk sets. Models should be fitted to the person-period dataset obtained from using the grouping of time that leads to the smallest number of risk sets (and hence the smallest person-period dataset) without changing the parameter estimates of coefficients. Alternatively an estimator adjusting for time aggregation bias, or the complementary log-log link function as opposed to the logistic, should be used.

The second alternative method to be considered involved aggregating the data of individuals within the same higher-level units, who had the same values for covariates included in a particular model. This implied that just one line of data represented all such individuals. Aggregating the data in this way can lead to a reduction in the size of the expanded dataset. Although it should be possible to fit both multilevel continuous-time and discrete-time survival models to the aggregated dataset, because the person-period dataset could not be created in MLwiN for the Swedish data when time was continuous, only discrete-time models could be fitted. This is because the aggregated dataset has to be constructed from the person-period dataset.

This method works best when there are a large number of individuals nested within each of the higher-level units, when the number of covariates to be grouped on is small and when covariates are categorical variables. Because all of these criteria were satisfied when aggregating the Swedish dataset, grouping the data in this way led to a large percentage reduction, over 50%, in the size of the person-period dataset before aggregation.

The final alternative method to be considered involved fitting Bayesian survival ‘frailty’ models in WinBUGS and using MCMC methods of estimation. In WinBUGS, an additive frailty model is adopted and a Weibull distribution is assumed for the survivor function. There are a number of reasons why this approach may be favoured over the others. Firstly, the Weibull model does not require the creation of a person-period dataset, and therefore there are no concerns over

the dataset becoming too large to work with. Recall that the Swedish dataset contained 185963 individuals, or 185449 individuals after excluding those with missing data. Secondly, time is treated as a continuous variable in the Weibull model, and thus there is no time aggregation bias implying that parameter estimates may be more accurate than when using discrete-time models. The Weibull model fitted to the Swedish dataset using MCMC estimation produced results which were consistent with those obtained from fitting the other alternative methods in MLwiN. However, as with the Scottish dataset, there was the problem of slow convergence for some parameters. A re-parameterised version of the Weibull model which incorporated a parameter expansion was adopted in an attempt to overcome these problems.

This section has detailed how well the three alternative methods performed when fitted to a large dataset. Recommendations for which of the three methods may be the most suitable, depending on, for example, the type of data, the research questions etc, are given in Chapter 10.

10 Discussion

10.1 Introduction

Event history models, or survival models, as they are more commonly referred to in medical applications, are applied when the outcome is a measure of duration. Therefore, they are important in the field of public health where it is often of interest to measure time until a particular pre-defined event occurs, such as death from some disease.

It is widely acknowledged that, for many outcomes, the health of individuals varies across geographical locations. Since this can also be true of event times, it is important that such survival data are analysed using multilevel survival models. These account for the dependence of event times nested within the same geographical location. Although multilevel survival models have been developed, computational requirements mean that their use is limited for large datasets. As discussed in Section 1.3, this poses a problem for those working in the field of public health since datasets for monitoring and measuring public health outcomes are typically large. Additionally, public health survival datasets may contain a large proportion of censored observations, because either the event of interest is rare or the period of follow-up is long. This poses a further problem since having many censored observations can also be troublesome when estimating multilevel survival models.

To recap from Section 1.3, the purpose of this thesis was to investigate ways in which multilevel survival models could be developed to model large datasets with a large proportion of censored observations. It is hoped that this will make them more accessible to those working in public health. Two datasets were employed for this purpose. The first was a moderately-sized Scottish dataset which was used as a training dataset to explore the limitations of existing software packages for fitting multilevel survival models, and then to develop alternative methods. Once alternative methods had been developed using this dataset, they were then applied to a second much larger dataset from Sweden to test how effective these alternative methods were when fitted to a larger

dataset. Section 10.2 provides a summary of methodological findings from the Scottish training dataset and the larger Swedish dataset.

10.2 Summary of Methodological Findings

A software package specially designed for fitting multilevel models to hierarchical data is MLwiN. Although fitting multilevel survival models is not a standard feature of MLwiN, macros are available for fitting two of the most commonly used survival models for modelling the effect of covariates on an outcome of duration. These are the proportional hazards model and the accelerated lifetime model. Because of the high proportion of censoring in the Scottish training dataset, a multilevel accelerated lifetime model could not be fitted for reasons discussed in Section 5.4.1. This meant that only the multilevel continuous-time proportional hazards model could be estimated in MLwiN for this dataset. Section 5.3.3.1 demonstrated how a proportional hazards model can be fitted via a Poisson model, which is the method adopted in MLwiN. This section also demonstrated how the person-period dataset required to fit the Poisson model could be created. This required that each individual's record be replicated as many times as the observed number of time points until either the event of interest or censoring occurred. As time is being treated as a continuous variable when fitting the Poisson model, creating the person-period dataset can lead to a vast expansion in the size of the original dataset, especially if the period of follow-up is long. Additionally, if the event of interest is rare, then the majority of individuals in the dataset would have a record of data corresponding to every continuous time point at which an event occurred. With the Scottish dataset, which originally consisted of 15305 individuals, creation of the person-period dataset led to an expanded dataset containing approximately 1.9 million observations within individuals.

MLwiN was able to cope with fitting the multilevel Poisson model to this size of dataset, the only problem being that the first-order PQL estimation procedure had to be used instead of the preferred second-order PQL procedure. However, since the Scottish dataset was only moderately-sized in the realm of public

health datasets, it was necessary to investigate other methods which could be used as an alternative to multilevel continuous-time models when datasets are much larger. Indeed, Section 9.4.1 revealed that the use of multilevel continuous-time models in MLwiN for the large Swedish dataset, which consisted of 185963 individuals, was impossible. This was because the dataset was too large to be expanded in order to create the person-period dataset to which the Poisson models are then fitted.

Three alternative methods were discussed in Chapter 7 and were applied to the Scottish training dataset, with results displayed in Chapter 8. Two of the alternative methods were applied in MLwiN; however, the third method involved fitting Bayesian multilevel survival (frailty) models in WinBUGS and using MCMC methods of estimation. The three alternative methods were then fitted to the Swedish dataset to test their suitability for modelling a much larger dataset (Chapter 9). The performance of these three methods when fitted to the both datasets is now considered.

The first alternative method, as discussed in Section 7.2, involved defining different risk sets and fitting discrete-time hazard models. Instead of treating time as a continuous variable, thus having to define a risk set for each time at which an event occurred, this method involved dividing time into discrete time intervals, either of equal or varying length. Dividing time like this led to a reduction in the number of risk sets, and thus a reduction in the size of the person-period dataset. On creation of the person-period dataset using this new discrete-grouping of time, standard methods for fitting multilevel models to discrete response data, such as logistic regression, could be employed. Indeed, it was the logistic link function that was used to fit the multilevel discrete-time model to the Scottish training dataset. Dividing time into discrete-time intervals, either when intervals were divided into equal lengths or varying lengths, constructed according to when events occurred, led to a vast reduction in the size of the continuous-time person-period dataset. The percentage reductions in the continuous-time person-period dataset were approximately 94% and 97% respectively when intervals were of equal and varying lengths. The discrete-time modelling approach also worked well when fitted to the large Swedish dataset, although various attempts at dividing up time had to be considered in order to find the smallest number of discrete-time intervals permitted, and hence the

smallest number of risk sets, without influencing estimates of coefficients. It was of interest to have fewer risk sets since this implies a smaller person-period dataset.

The second alternative method, as discussed in Section 7.3, was termed ‘grouping according to covariates’, and involved aggregating the data of individuals within the same higher-level units who had the same values for covariates included in a particular model so that one line of data was used to represent all such individuals. The concept behind this method is that all individuals within the same geographical location with the same values for covariates included in a particular model are at risk of experiencing the event of interest at the same time. As a result, all of these individuals can be represented by one line of data. Aggregating the data in this way can lead to a reduction in the size of the expanded dataset. The multilevel continuous-time and discrete-time survival models employed by MLwiN can be adapted to model the aggregated dataset. This was covered in Sections 7.3.2 and 7.3.3. Both continuous-time and discrete-time models were fitted to the aggregated Scottish dataset. When time was treated as continuous, implying a risk set for each distinct event time, aggregating the dataset reduced the size of the continuous-time person-period dataset (before aggregation) by between 4% and 84%. This depended upon how many covariates were used for the grouping. Time was then treated as discrete and, although the widths of the intervals could be equal or varying, the most successful percentage reduction in the continuous-time Scottish person-period dataset occurred when intervals were varying in length, leading to a reduction of between 97% and 99.5%. Again, this percentage depended upon how many covariates were used for the grouping. This method also worked well when fitted to the large Swedish dataset; however, because the aggregated dataset must be created using the person-period dataset, only discrete-time models could be fitted to the Swedish dataset since it was too large to create the person-period dataset when time was continuous. When time was discrete, grouping according to all individual- and higher-level covariates led to a reduction of over 50% in the discrete-time person-period dataset before aggregation.

The final alternative method to be considered involved fitting Bayesian survival ‘frailty’ models in WinBUGS and using the MCMC method of estimation, as

discussed in Section 7.4. In WinBUGS, an additive frailty model is adopted and a Weibull distribution is assumed for the survivor function. It was shown that the regression parameter estimates obtained from the Weibull model could be interpreted as hazard ratios; hence they were comparable with those obtained from fitting the continuous-time Poisson model. However, when fitting frailty models to the Scottish dataset, although parameter estimates of fixed and random effects obtained from the Weibull model were very similar to those obtained using the Poisson model in MLwiN, trace plots revealed some poor mixing of Markov chains for some parameters, as well as the Gibbs sampler tending to get trapped near zero for the random-effects variance. It was hypothesised that the high percentage of censored observations could be the root of the problems, with the Weibull model failing to provide a good fit in the presence of many censored observations. However, a simulation study revealed that the high percentage of censoring only slightly affected parameter estimates, and could not explain the poor mixing of Markov chains for some parameters. Therefore, it was necessary to consider, instead, a re-parameterised version of the Weibull model, which also included a parameter expansion to help speed up convergence for the random-effects variance. Similar problems were encountered when fitting the Bayesian frailty model to the Swedish dataset; therefore the re-parameterised Weibull model with the parameter expansion was considered for this dataset also. As with the Scottish dataset, using the re-parameterised version of the Weibull model successfully improved the poor mixing and reduced the correlation in the chains for the intercept and the shape parameter of the Weibull distribution. Furthermore, using the variance expansion technique appeared to be more effective at speeding up convergence for the higher-level variance when fitted to the Swedish dataset than it had been when used in the Weibull model fitted to the Scottish dataset.

There were further points for consideration when the Weibull model was fitted to the Swedish dataset. Unlike the Scottish dataset, for which the proportional hazards assumption had been reasonable, there was evidence of time-varying covariates in the Swedish dataset. When fitting either the continuous-time or discrete-time hazard model in MLwiN, time-varying covariates are easily incorporated by including an interaction between the time-dependent variable

and the baseline hazard function. However, in the Weibull model this could prove to be problematic as the baseline hazard function is restricted to be monotonically increasing, decreasing or constant [263]. A possible solution would be to use the piecewise Weibull model. The piecewise Weibull model allows the Weibull baseline hazard function to change at unknown change points [263]. Tarrés et al. [264] and Casellas [263] demonstrated how the inclusion of time-varying covariates converted the Weibull hazard function into a piecewise Weibull (or Weibull time-dependent) hazard function. They showed how a different slope is defined for each period of time, where the cut-point (or change point) of the time period can be established either using a spline regression [264] or treating them as unknown parameters in the model to be estimated [263]. The differing slopes represent the differing hazards in each time period.

10.3 Conclusions

This thesis has considered a number of ways in which multilevel survival models can be fitted to large datasets with a high percentage of censored observations. Based on the results from each of these methods, as summarised in Section 10.2, this section will provide recommendations on the effectiveness of each method by considering the advantages and disadvantages of each.

Fitting a Poisson model in MLwiN may seem like an appealing option since, after creation of a person-period dataset, the (exponentials of) regression parameters in the Poisson model provide identical estimates of hazard ratios obtained from proportional hazards models. In addition, there is no time-aggregation bias when time is treated as continuous, since each distinct event time corresponds to a separate risk set. However, although this method is effective for small to moderately sized datasets, this thesis has shown that it fails when fitted to large datasets. As a result, fitting multilevel Poisson models in MLwiN would not be recommended to those working in the field of public health, where datasets typically tend to be large in size, unless they are sure that the dataset in question is small enough to be expanded for creation of the person-period

dataset. An alternative continuous-time model which can be implemented in MLwiN is the accelerated lifetime model. This approach may be more favourable than the Poisson modelling approach as no data expansion is required to fit the accelerated lifetime model. However, it is recommended that this model is not used if at least half of the observations in the dataset are censored. This is because estimation procedures used in MLwiN to estimate non-linear models (quasi-likelihood under IGLS) are prone to breaking down for this model when there is a high proportion of censored observations. As a result, the accelerated lifetime model may also not be recommendable to those working in public health, unless the outcome of interest and the length of follow-up time are such that no more than fifty percent of observations in a dataset are censored.

Fitting discrete-time models in MLwiN can be a useful alternative to fitting continuous-time models. Because risk sets correspond to discrete-time intervals instead of each distinct event time, the size of the person-period dataset also required to fit these models can be greatly reduced. On creation of the person-period dataset, fitting discrete-time models in MLwiN is straightforward since standard approaches to modelling discrete response data, such as logistic regression, may be used. Other advantages of the discrete-time approach include that it can easily incorporate tied observations and time-varying covariates. There are, however, some potential problems with this method which must be considered before using it for data analysis.

One potential problem with using the discrete-time model is that estimates of coefficients depend on the length of time interval when the logistic link function is used; therefore, estimates from this model may not be completely identical to those obtained from fitting a continuous-time model. However, if the width of each discrete-time interval is small enough, then the logistic model converges to the proportional hazards model, meaning estimates of coefficients will be more similar. Therefore, when using this method, it is necessary to experiment with the widths of the discrete-time intervals in order to find a trade-off between having the smallest number of discrete-time intervals, and hence the smallest number of risk sets, so that the size of the person-period dataset is as small as possible without influencing coefficient estimates. If using the discrete-time approach, it may be advisable to, first, run a single-level proportional hazards model to get a rough idea of parameter estimates. This will determine whether

estimates obtained using the discrete-time approach are being influenced by the length of the time intervals. Alternatively, an adjustment for time-bias could be included, or the complementary log-log link could be used as opposed to the logistic. Use of the complementary log-log link was not considered here because of time constraints, and also because of the computational convenience and easier interpretation when the logistic function is used, thus making its use more desirable.

When fitting multilevel survival models in MLwiN, either using the continuous-time Poisson modelling approach or the discrete-time modelling approach, the size of the person-period dataset required for both methods can be reduced further by grouping according to covariates. However, as discussed throughout this thesis, this method is not the easiest to implement for a number of reasons. Firstly, the aggregated dataset has to be re-created each time the covariates in a particular model change. As a result, this method would not be recommended for model selection. Secondly, the effectiveness of this method at reducing the size of the person-period dataset depends largely on the number of covariates to be grouped on and the number of individuals within each higher-level unit. If on average there are a large number of individuals clustered within each higher-level unit, then there is a greater chance that there will be more individuals within that higher-level unit sharing the same values for the covariates to be grouped on. This would lead to a greater reduction in the person-period dataset and vice versa. Ultimately, however, it is clear that, regardless of the number of individuals per higher-level unit, the number of individuals with identical covariates becomes smaller as the number of covariates to be grouped on increases. Further to this, if risk factors are measured on a continuous scale, the number of individuals sharing exact values for continuous risk factors will decrease as the number of continuous risk factors to be grouped on increases. It should be noted also that, because the aggregated dataset must be constructed from the person-period dataset, only discrete-time models can be used if a dataset is very large for reasons discussed earlier in this section.

Although there are many issues which must be considered before adopting the grouping according to covariates method, it can be very effective in reducing the size of the person-period dataset, as demonstrated with both the Scottish and Swedish datasets. Once a final model has been selected, provided that there

are, on average, a large number of individuals per higher-level unit, not too many covariates in the final model, and that the majority of covariates are categorical, this method can lead to a vast reduction in the size of the person-period dataset before aggregation. As a result more preferable methods of estimation in MLwiN, such as second-order PQL, may become available due to the reduction in the size of the person-period dataset.

An entirely different approach which may be adopted is to fit Bayesian survival (frailty) models and use MCMC methods of estimation. Such models can be easily implemented in WinBUGS, a package designed specially to make practical MCMC methods available to applied statisticians. There are a number of reasons why a Bayesian approach may be preferred over a traditional frequentist approach. Firstly, the Bayesian approach allows any prior knowledge about parameters to be incorporated into analysis. This may be useful in the field of public health if a particular research problem has been considered before in previous studies meaning that prior information is available on the parameters of interest. Secondly, with the recent advances in computing technology, Bayesian inference using MCMC allows more complex models to be fitted straightforwardly.

More specifically, however, there are also reasons why fitting multilevel survival models in WinBUGS may be preferred to MLwiN. Unlike the approaches adopted in MLwiN in this thesis, fitting frailty models in WinBUGS does not require creation of a person-period dataset, and thus there is no issue of a dataset becoming too large to work with following expansion. Also, time is treated as continuous when fitting frailty models in WinBUGS implying that there are no concerns over time-aggregation bias. Lastly, there is also much more flexibility in the choice of frailty distribution in WinBUGS than in MLwiN. The frailty is the exponential of the random effects and in MLwiN it is constrained to follow a log-Normal distribution, whereas any distribution can be selected for this term in WinBUGS.

Although fitting Bayesian survival models in WinBUGS may seem like a more appealing approach than fitting these models in MLwiN, there are some drawbacks to the Bayesian approach. Estimating models using MCMC can take longer than estimating the same models using quasi-likelihood methods. Although various techniques such as re-parameterisation and parameter

expansion can be employed to speed up convergence with the aim of reducing computing time, if quick estimation of models is required, this would not be the best approach. This is especially a problem when the dataset in question is large, and also if there are a lot of covariates in the model. However, if computing time is not important, then this approach, due to its greater flexibility, may be more favourable than the frequentist approaches.

This thesis has shown that there are a number of efficient methods which can be used to model large, hierarchically-structured, survival datasets as an alternative to continuous-time models. However, before selecting one of these approaches, public health researchers should first consider what the main objectives of the research are. If interest lies in quickly analysing a dataset to determine associations between covariates and event times, then the discrete-time approach in MLwiN may be desirable as models can be estimated quickly and straightforwardly using, for example, logistic regression models fitted to a person-period dataset. It may also be possible to reduce the size of the person-period dataset by grouping according to covariates. The frailty modelling approach in WinBUGS would not be favourable here as models take a long time to run using MCMC when datasets are large. However, if computing time is not an issue, then fitting frailty models in WinBUGS may be more desirable because of the greater flexibility in using a Bayesian approach. Furthermore, parameter estimates may be more accurate since time is treated as continuous, and thus there are no concerns over time-aggregation bias.

10.4 Implications of the Findings

In the past, the use of multilevel survival models in the field of public health has been limited because datasets used for measuring and monitoring public health are typically large. Large datasets pose a problem when trying to fit commonly used multilevel survival models such as the proportional hazards models, in conventional multilevel software packages such as MLwiN. This thesis has introduced alternative approaches which can be employed to make multilevel survival models more accessible to those working in public health, and this

section considers what the research in this thesis has contributed to the wider literature.

In Chapter 5, forty papers fitting multilevel survival models to real datasets were reviewed; not all were public health datasets. From these forty papers, ten were selected as meeting the criteria for being classed as large datasets. To meet these criteria, the datasets in question had to either consist of more than 15305 individuals and/or have a follow-up period of more than 9 years. These conditions were defined as it had already been demonstrated using the Scottish dataset that multilevel proportional hazards models, estimated via Poisson models in MLwiN, could be fitted without any problems to datasets of this size. Therefore, it was not of interest to consider datasets smaller than this. Of the ten papers reviewed, the authors had considered various options to fit multilevel survival models to their datasets. MLwiN was the most commonly used package, with half of the papers using it to fit the models. Most authors using MLwiN stratified analysis by breaking-up the datasets into smaller cohorts in order to make the person-period dataset of a more manageable size for fitting proportional hazards models. This thesis has introduced methods which do not require the need to break up datasets in order to fit multilevel survival models.

Another of the papers that used MLwiN implemented the accelerated lifetime model; however, as discussed throughout this thesis, the use of MLwiN to estimate this model is not recommended if there is a high proportion of censored observations. This can occur in public health if the event of interest is rare. This thesis has considered models which can still be easily estimated, even when the proportion of censored observations is high.

One of the reviewed papers was able to successfully implement the proportional hazards model on a very large dataset using the R software package. This could be yet another alternative way of fitting continuous-time models as opposed to using MLwiN or WinBUGS; however, it was noted that R can only be used to fit multilevel models when there is just one random effect. For many public health datasets, there may be more than one higher level, as with the Swedish dataset in this thesis; thus the use of R would not be suitable. This thesis has introduced methods which can incorporate more than one random effect.

Only one of the reviewed papers adopted a Bayesian approach to fitting multilevel survival models. Authors fitted an additive frailty model in WinBUGS, the same approach as taken in this thesis. This thesis aims to assist in increasing the awareness of public health researchers to the possibility of using Bayesian survival (frailty) models as an alternative to traditional frequentist approaches.

To summarise, this thesis has attempted to contribute to the wider literature by introducing approaches for dealing with many of the problems posed by public health datasets. For example, it has shown that multilevel survival models can still be fitted when datasets are large, when there is a high percentage of censored observations and when there is more than one higher level. It has also highlighted the possibility of using a Bayesian approach instead of traditional frequentist methods.

10.5 Limitations and Recommendations

This section will summarise the methodological limitations of this research and recommend areas for further work based on these limitations. Limitations concerning the datasets used in this thesis will not be considered here since this has already been covered in Chapter 6 for the Scottish data and in Section 9.5.2 for the Swedish data.

10.5.1 Methodological Limitations and Recommendations

For each of the four methods employed for fitting multilevel survival models in this thesis, i.e. the Poisson, discrete-time and grouping according to covariates modelling in MLwiN, and the frailty modelling approach in WinBUGS, Section 10.3 gave a detailed account of the advantages and disadvantages of each. The disadvantages may be seen as limitations of using these methods. For example, Section 10.3 discussed that, when fitting discrete-time models, it is advisable to experiment with the widths of the discrete-time intervals in order to find a trade-off between having the smallest number of discrete-time intervals, and

hence the smallest number of risk sets so that the size of the person-period dataset is as small as possible without influencing coefficient estimates. This implies having to create a new person-period dataset for each different division of time being considered, as well as having to run models using each different division of time in order to compare estimates of coefficients from each. Therefore, in practice, this method has the potential to be quite cumbersome.

For the grouping according to covariates approach, Section 10.3 discussed how this method is most suitable when there are a large number of individuals nested within each of the higher-level units, when the number of covariates to be grouped on is small, and when covariates are categorical variables. These can be a lot of conditions to satisfy, and therefore this method may not prove very efficient in a lot of circumstances. This could be particularly true if using this method for applications outside public health. In public health and epidemiology, a lot of data on risk factors tends to be categorical; however, this may not be the case in other fields of research.

The biggest limitation with using Bayesian methods, as highlighted in Section 10.3, is the time taken to run models when using MCMC methods of estimation, especially when datasets are large or there are a lot of covariates to be included in the model. Another limitation which can increase the time taken to draw final conclusions from Bayesian models is that models should be run with different priors on the parameters. Repeatedly running models in order to test the use of different prior distributions will increase the overall computing time. In this thesis, vague priors were adopted so as not to have any influence on the results. Therefore, in order to check that the choice of prior distribution was not affecting results, a sensitivity analysis should have been performed. This was not performed here due to time constraints on the thesis, and also because parameter estimates obtained from the Bayesian models were similar to those obtained from the frequentist models. However, if only adopting Bayesian models, then it would be advisable to perform a sensitivity analysis using different prior distributions.

10.5.2 Other Limitations

In Section 4.1.3 it was acknowledged that the multiple linear regression technique used for imputing missing values in the SHeS dataset was not the most sophisticated means of imputing data. Similarly, for the Swedish dataset, Section 9.3.2 discussed that no method of imputation was used to impute missing data and therefore, any individuals with missing data were excluded from analyses.

Excluding cases with missing data, as was the method used when analysing the Swedish dataset, is not advisable since this can affect inferences drawn from analyses. Fayers et al. [144] discussed the three main consequences of ignoring missing data, which included loss of power and biased estimates of associations. Additionally, excluding cases with missing data could lead to having insufficient data to form any sensible conclusions from analyses. This was not an issue with the Swedish dataset, although it could become more of a problem for a smaller dataset with a lot of missing data. However, it is not advisable to ignore missing data, even when the proportion of missing data is small, since it is known that bias can still occur. Excluding cases with missing data, known as ‘listwise’ or ‘case’ deletion is the most commonly used approach to missing data, and is the option used by statistical software packages. Acock [148] detailed the disadvantages with this method.

When analysing the Scottish data, some attempt was made to impute missing values using single imputation via multiple linear regression. Although this is much more favourable than case deletion, there are still some drawbacks with this method as opposed to more sophisticated methods. Acock [148] described how single imputation can underestimate standard errors, thereby overestimating the level of precision. Instead, multiple imputation would have been the preferred method for imputing missing values in this thesis. Multiple imputation generates a defined number of separate datasets. Parameter estimates from each can be pooled together to provide an improved estimate [148]. Multiple imputation was not used in this thesis due to time constraints; however, if results were going to be submitted for publication, then it may be advisable to use a more sophisticated method, such as multiple imputation.

10.5.3 Other Recommendations

The following are not recommendations based on limitations of this research, but are instead ways in which the research in this thesis could be extended.

In this thesis, interest has been confined to observing the time until an event occurs for the first time. For example, with the Scottish dataset, interest was in measuring the time until first psychiatric admission during follow-up; however, in this example, and in many other public health applications, it is possible that an individual could experience the event of interest more than once. In the case of the Scottish data, this would be the form of a readmission to psychiatric facilities during follow-up. Obviously, there are some cases in which more than one occurrence of an event would be impossible, for example, if the outcome of interest was death from some disease. However, for situations where more than one event of interest is possible, these ‘repeated events’ are usually handled by including individual-specific random effects in a survival model. The random effects account for the correlation in the durations between events due to the presence of unobserved individual-level factors [208].

Other common features of survival models can include multiple states; for example, ‘diseased’ or ‘not diseased’. An event would then be a transition between states. Another feature is competing risks, which refers to when there are multiple types of event. For information on how to model repeated events, multiple states and/or competing risks refer to Steele et al. [265], Steele et al. [174], Goldstein et al. [266], Steele et al. [208] and references therein.

Appendix 1: 12-Item General Health Questionnaire (GHQ-12)

Have you recently?

1.	Been able to concentrate on what you're doing?	Better than usual	Same as usual	Less than usual	Much less than usual
2.	Lost much sleep over worry?	Not at all	No more than usual	Rather more than usual	Much more than usual
3.	Felt you were playing a useful part in things?	More so than usual	Same as usual	Less useful than usual	Much less useful
4.	Felt capable of making decisions about things?	More so than usual	Same as usual	Less so than usual	Much less capable
5.	Felt constantly under strain?	Not at all	No more than usual	Rather more than usual	Much more than usual
6.	Felt you couldn't overcome your difficulties?	Not at all	No more than usual	Rather more than usual	Much more than usual
7.	Been able to enjoy your normal day-to-day activities?	More so than usual	Same as usual	Less so than usual	Much less than usual
8.	Been able to face up to your problems?	More so than usual	Same as usual	Less so than usual	Much less able
9.	Been feeling unhappy and depressed?	Not at all	No more than usual	Rather more than usual	Much more than usual
10.	Been losing confidence in yourself?	Not at all	No more than usual	Rather more than usual	Much more than usual
11.	Been thinking of yourself as a worthless person?	Not at all	No more than usual	Rather more than usual	Much more than usual
12.	Been feeling reasonably happy, all things considered	More so than usual	About same as usual	Less so than usual	Much less than usual

Source: www.bris.ac.uk/poverty/pse/99-Pilot/99-Pilot_4.doc

Appendix 2: Checking the Proportional Hazards Assumption in the SHeS Data

As discussed in Section 5.3.3.4, the proportional hazards assumption can be checked by including an interaction term between each variable of interest and the variable for time. A non-significant interaction signifies that the proportional hazards assumption is satisfied. The table below presents parameter estimates obtained from fitting a two-way interaction between the logarithm of time and each of the fixed effects included in the continuous-time model with all significant risk factors (model B3 in Table 5.3). Note that the two-way interactions were fitted one at a time and not all at once. Note also that only the estimates for the interaction terms are given here. For all other parameter estimates refer to Table 5.3. Estimates were obtained using 1st-order PQL.

Two-way interaction	Estimate (s.e.)	p-value for interaction
GHQ-12*log(t)		
Score 0	0.000	0.971
Score 1-2*log(t)	0.217 (0.244)	
Score 3-4*log(t)	-0.083 (0.259)	
Score 5-12*log(t)	-0.022 (0.209)	
Sex*log(t)		
Male	0.000	0.599
Female*log(t)	-0.089 (0.170)	
Age*log(t)		
16-24	0.000	0.997
25-34*log(t)	-0.160 (0.261)	
35-44*log(t)	-0.009 (0.263)	
45-54*log(t)	0.251 (0.355)	
55-64*log(t)	0.222 (0.304)	
65-74*log(t)	0.538 (0.466)	
Marital Status*log(t)		
Married/Cohabiting	0.000	0.856
Other marital*log(t)	-0.031 (0.169)	
Benefits*log(t)		
No benefits	0.000	0.755
Yes benefits*log(t)	0.053 (0.171)	
Smoking Status*log(t)		
Non-Smoker	0.000	0.351
Current smoker*log(t)	-0.065 (0.201)	
Ex-smoker*log(t)	0.608 (0.396)	
Employment Status*log(t)		
Full-time	0.000	0.999
Part-time*log(t)	0.008 (0.234)	
Unemployed*log(t)	0.037 (0.238)	

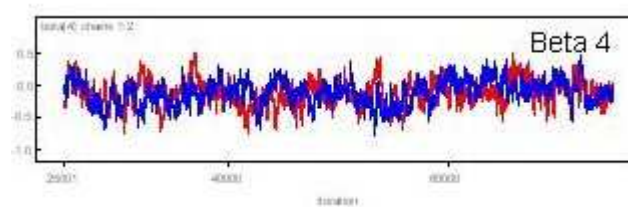
Self-Assessed Health*log(t)		
Very good	0.000	
Good*log(t)	-0.554 (0.275)	0.462
Fair*log(t)	-0.672 (0.277)	
Bad*log(t)	-0.996 (0.445)	
Very bad*log(t)	0.717 (0.777)	

It can be seen from the table above that the proportional hazards assumption is satisfied for all covariates.

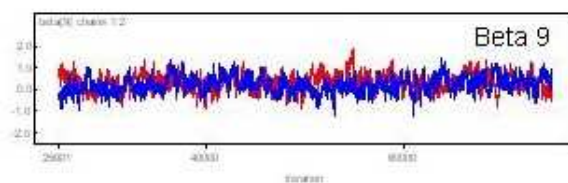
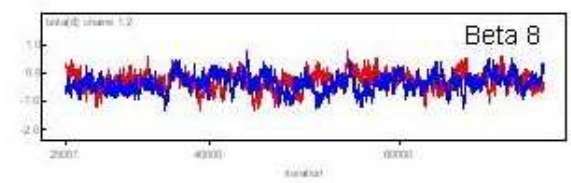
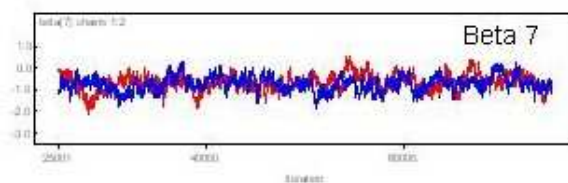
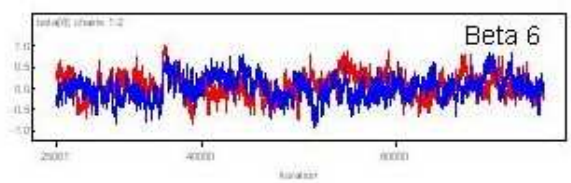
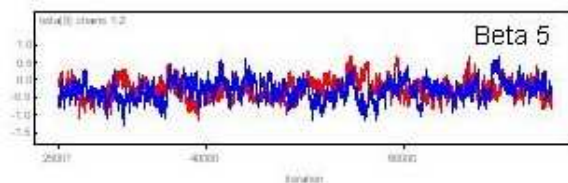
Appendix 3: Trace Plots and Gelman-Rubin Plots from SHeS Weibull Model

When fitting the Weibull model with all significant covariates to the SHeS dataset, Section 8.3.2.1 only displayed trace plots and Gelman-Rubin plots for the intercept, GHQ-12 regression parameters, shape parameter and random effects variance. Trace plots and Gelman-Rubin plots for the other regression parameters in the model are given below.

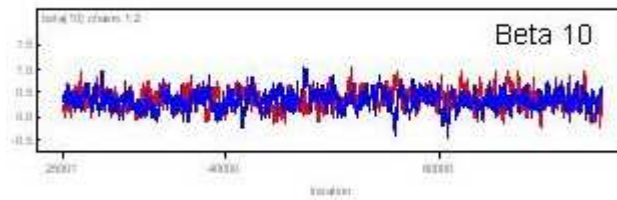
Trace Plots



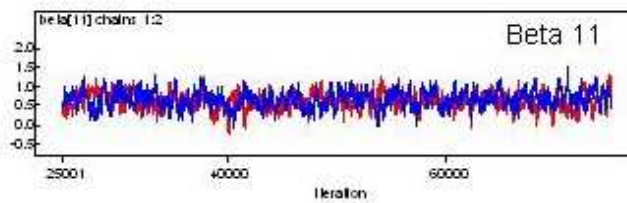
Sex



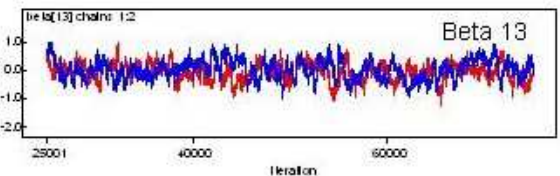
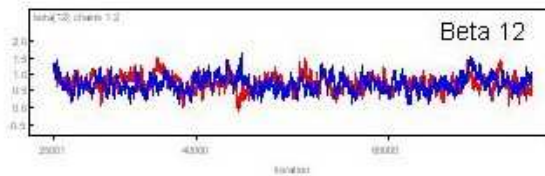
Age



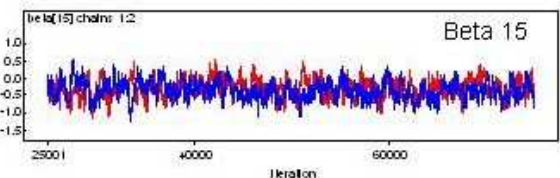
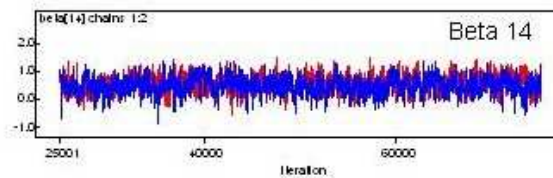
Marital Status



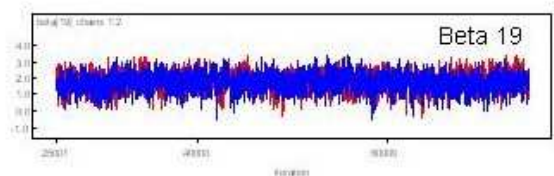
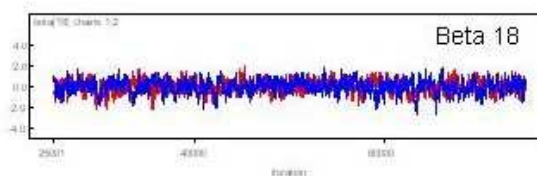
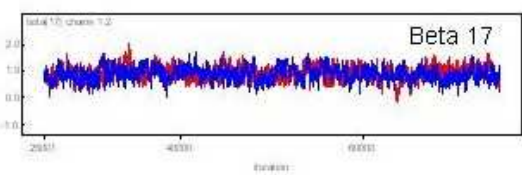
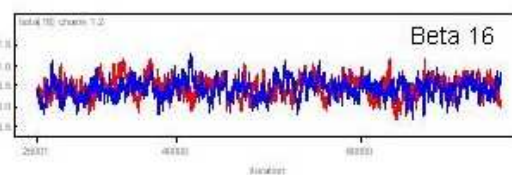
Receipt of Benefits



Smoking Status

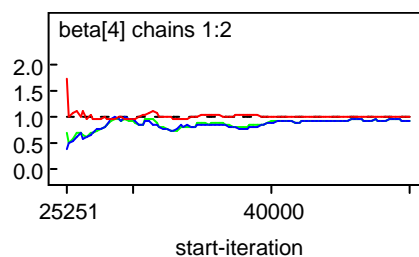


Employment Status

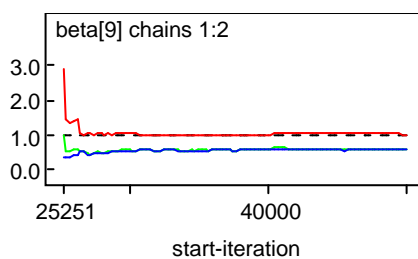
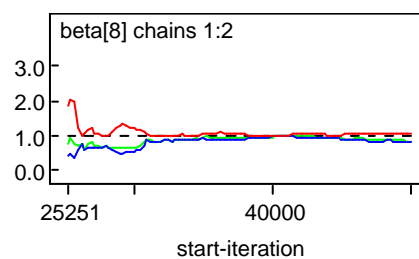
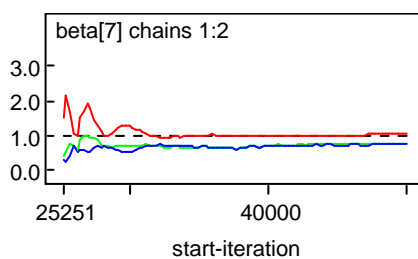
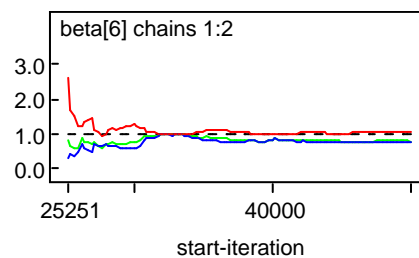
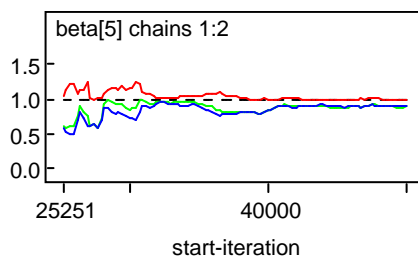


Self-Assessed General Health

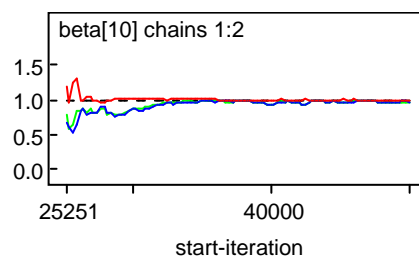
Gelman-Rubin Plots



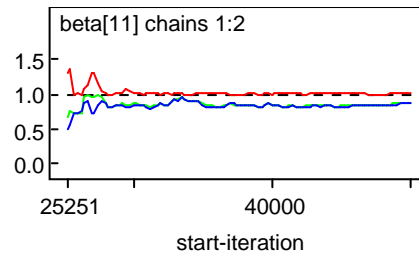
Sex



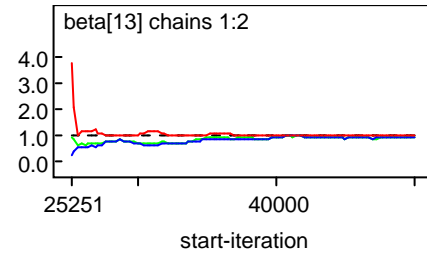
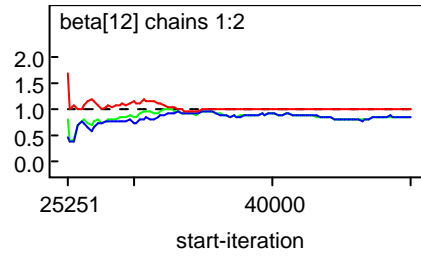
Age



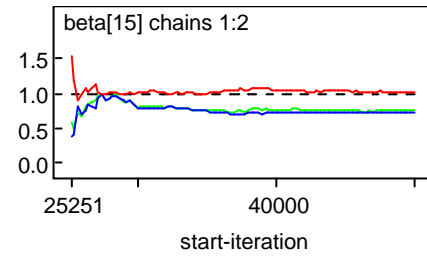
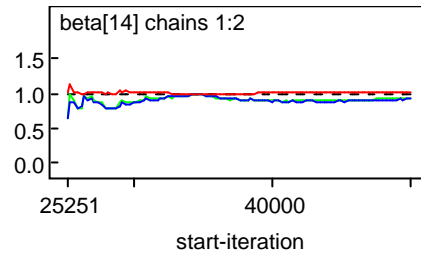
Marital Status



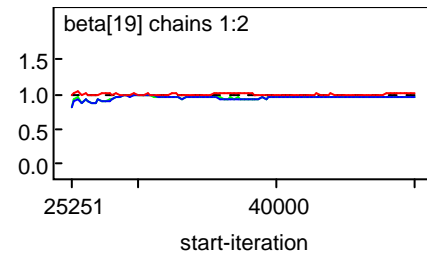
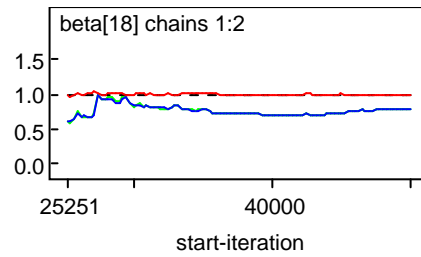
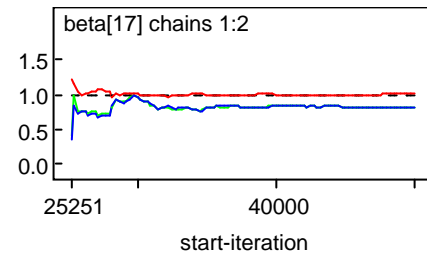
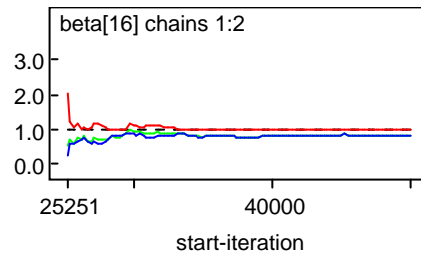
Receipt of Benefits



Smoking Status



Employment Status



Self-Assessed General Health

Appendix 4: WinBUGS Code for Re-parameterised Model with all Covariates

The WinBUGS code for the re-parameterised Weibull model containing all significant covariates, i.e. the ‘full’ model, in Section 8.3.4 is given below.

```
Model
{
  for (i in 1:N) {
    time[i] ~ dweib(r,mu[i])|(censor[i],)
    log(mu[i]) <- -r*log(lambda[i])
    + u2[area[i]]
  }
  # Random effects:
  for (j in 1:n2){
    u2[j] ~ dnorm(0.0, tau.u2)
  }
  # Priors:
  loglambda1 ~ dnorm(0, 0.1)
  for (k in 1:19){
    loglambda2[k] ~ dnorm(0, 0.1)
  }
  for (i in 1:N) {
    loglambda[i] <- loglambda1 + loglambda2[1]*score_1_2[i] + loglambda2[2]*score_3_4[i] +
    loglambda2[3]*score_5_12[i] + loglambda2[4]*female[i] + loglambda2[5]*v25_34[i] +
    loglambda2[6]*v35_44[i] + loglambda2[7]*v45_54[i] + loglambda2[8]*v55_64[i] +
    loglambda2[9]*v65_74[i] + loglambda2[10]*other_marital[i] + loglambda2[11]*yes_benefits[i] +
    loglambda2[12]*currentsmok[i] + loglambda2[13]*exsmok[i] +
    loglambda2[14]*unemployed[i] + loglambda2[15]*part_time[i] + loglambda2[16]*good[i] +
    loglambda2[17]*fair[i] + loglambda2[18]*bad[i] + loglambda2[19]*very_bad[i]
    lambda[i] <- exp(loglambda[i])
  }
  alpha <- -(r*loglambda1)
  beta[1] <- -(r*loglambda2[1])
  beta[2] <- -(r*loglambda2[2])
  beta[3] <- -(r*loglambda2[3])
  beta[4] <- -(r*loglambda2[4])
  beta[5] <- -(r*loglambda2[5])
  beta[6] <- -(r*loglambda2[6])
  beta[7] <- -(r*loglambda2[7])
  beta[8] <- -(r*loglambda2[8])
  beta[9] <- -(r*loglambda2[9])
  beta[10] <- -(r*loglambda2[10])
  beta[11] <- -(r*loglambda2[11])
  beta[12] <- -(r*loglambda2[12])
  beta[13] <- -(r*loglambda2[13])
  beta[14] <- -(r*loglambda2[14])
  beta[15] <- -(r*loglambda2[15])
  beta[16] <- -(r*loglambda2[16])
  beta[17] <- -(r*loglambda2[17])
  beta[18] <- -(r*loglambda2[18])
  beta[19] <- -(r*loglambda2[19])
  # Priors for random effects variance
  sigma.u2 ~ dunif(0,3)
  sigma2.u2 <- sigma.u2*sigma.u2
  tau.u2 <- 1/sigma2.u2
}
```

```
#Prior on shape parameter
logr ~ dnorm(0, 0.1)
r <-exp(logr)
}
```

Appendix 5: Discrete-Time Groupings for Swedish Dataset

The following two tables display the discrete-time groupings of days used to create the Swedish person-period dataset with 5 risk sets and 10 risk sets respectively. The groupings for the person-period datasets with 3 and 7 risk sets were given in Tables 9.5 and 9.6 respectively.

Discrete-time grouping for expanded dataset with 5 risk sets

Time Interval	Grouping
1	Day 0 – day 1700
2	Day 1701 – day 2700
3	Day 2701 – day 4500
4	Day 4501 – day 6100
5	Day 6101 – day 8373
6	Day 8374 – day 8500

Note that, although there are 6 discrete-time intervals in the above table, the last time interval contains only censored observations, and therefore was not included as a risk set since no events occurred during that interval.

Discrete-time grouping for expanded dataset with 10 risk sets

Time Interval	Grouping
1	Day 0 – day 900
2	Day 901 – day 1700
3	Day 1701 – day 2700
4	Day 2701 – day 3500
5	Day 3501 – day 4500
6	Day 4501 – day 5100
7	Day 5101 – day 6100
8	Day 6101 – day 6700
9	Day 6701 – day 7300
10	Day 7301 – day 8373
11	Day 8374 – day 8500

Note that, although there are 11 discrete-time intervals in the above table, the last time interval contains only censored observations, and therefore was not

included as a risk set since no events occurred during that interval. Note that the 9th and 10th risk sets contain information on events for individuals from the older 1972 birth cohort only, as the last censored observation in the 1977 cohort occurred at 6559 days from 12th birthday.

Appendix 6: Checking the Proportional Odds Assumption in the Swedish Dataset

Section 7.2.3 noted that fitting discrete-time models requires a proportionality assumption, which is referred to as the ‘proportional odds’ assumption if the logit link function is adopted. As with the proportional hazards assumption, this can be checked by including two-way interactions between covariates and time in the model of interest in order to check that the effect of the covariate is the same at all time points. A non-significant interaction implies the proportionality assumption is reasonable.

The table below displays parameter estimates obtained from fitting a two-way interaction between time and each of the fixed effects included in the discrete-time ‘Individual+Area’ model fitted to the Swedish person-period dataset in Section 9.4.2. Note that the two-way interactions were fitted one at a time and not all at once. Note also that only the estimates for the interaction terms are given here. For all other parameter estimates refer to Table 9.7. Since it was already established in Table 9.8 that the effect of ‘cohort’ was not constant over time, it is not necessary to check the proportionality assumption for this variable again here. In order to cut down on the number of parameters to be estimated, the models including the two-way interactions were fitted to the person-period dataset with 3 risk sets. Although it was discussed that the baseline hazard function wasn’t being estimated very accurately when there were only 3 risk sets, it is hoped, nevertheless, that a rough indication of whether or not the effects of the covariates are constant over time will be obtained. Estimates were obtained using 2nd-order PQL.

Two-way interaction	Estimate (s.e.)
Sex*Time	
<i>Male*Time 1</i>	0.000
<i>Female*Time 2</i>	-0.547 (0.095)
<i>Female*Time 3</i>	-1.022 (0.092)
Father Soc. Class*Time	
<i>Employers etc*Time 1</i>	0.000
<i>Non-manual*Time 2</i>	0.207 (0.173)
<i>Manual*Time 2</i>	0.184 (0.166)
<i>Unclassifiable*Time 2</i>	0.050 (0.176)
<i>Non-manual*Time 3</i>	0.024 (0.172)

<i>Manual*Time 3</i>	0.204 (0.163)
<i>Unclassifiable*Time 3</i>	0.251 (0.170)
<hr/>	
Income Quintile*Time	
<i>Quintile 1*Time 1</i>	0.000
<i>Quintile 2*Time 2</i>	0.051 (0.136)
<i>Quintile 3*Time 2</i>	0.166 (0.142)
<i>Quintile 4*Time 2</i>	-0.166 (0.143)
<i>Quintile 5*Time 2</i>	0.221 (0.156)
<i>Missing*Time 2</i>	0.038 (0.175)
<i>Quintile 2*Time 3</i>	-0.037 (0.132)
<i>Quintile 3*Time 3</i>	0.125 (0.137)
<i>Quintile 4*Time 3</i>	-0.200 (0.139)
<i>Quintile 5*Time 3</i>	-0.024 (0.156)
<i>Missing*Time 3</i>	-0.086 (0.172)
<hr/>	
Housing Tenure*Time	
<i>Owner Occupied*Time 1</i>	0.000
<i>Rented*Time 2</i>	-0.120 (0.089)
<i>Rented*Time 3</i>	0.111 (0.087)
<hr/>	
Economic Region*Time	
<i>Metropolitan*Time 1</i>	0.000
<i>Larger Regional*Time 2</i>	0.159 (0.099)
<i>Smaller Regional*Time 2</i>	-0.173 (0.145)
<i>Private Enterprise*Time 2</i>	-0.162 (0.233)
<i>Public Sector*Time 2</i>	0.769 (0.321)
<i>Larger Regional*Time 3</i>	0.082 (0.098)
<i>Smaller Regional*Time 3</i>	-0.038 (0.136)
<i>Private Enterprise*Time 3</i>	-0.161 (0.226)
<i>Public Sector*Time 3</i>	0.184 (0.352)

Generally, the proportional odds assumptions seem reasonable for the variables ‘father’s social class in 1980’, ‘household income quintile at birth’ and ‘economic region’. However, there are significant two-way interactions between sex and time and housing tenure at birth and time, indicating that the proportionality assumption is not valid for these variables. This would suggest that these two-way interaction terms should be included in the final model.

Appendix 7: Fitting a Discrete-Time Model with Five Risk Sets to the Swedish Dataset

Section 9.4.2 noted that discrete-time models were also fitted to a person-period dataset containing 5 risk sets. A table indicating how the time intervals were constructed to create the 5 risk sets is given in Appendix 5. Results from fitting the ‘Individual’, ‘Individual+Area’ and ‘Full’ models to the Swedish data are given in the table below. Parameter estimates should be compared to those in Table 9.7. Models were estimated using 2nd-order PQL.

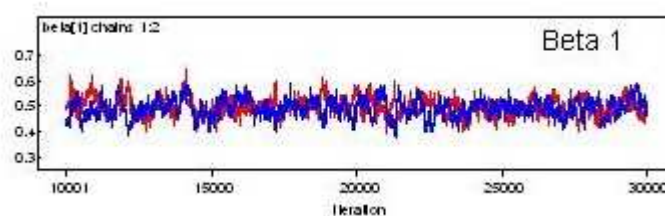
	Varied Intervals with 5 Risk Sets		
	Individual Estimate (s.e.)	Individual+Area Estimate (s.e.)	Full Estimate (s.e.)
Fixed			
Intercept (β_0)	-6.393 (0.080)	-6.357 (0.090)	-6.152 (0.108)
Time2 (α_1)	0.349 (0.058)	0.351 (0.062)	0.351 (0.062)
Time3 (α_2)	0.747 (0.054)	0.769 (0.057)	0.769 (0.057)
Time4 (α_3)	0.342 (0.054)	0.355 (0.062)	0.356 (0.062)
Time5 (α_4)	-0.067 (0.064)	-0.066 (0.068)	-0.066 (0.068)
Sex			
Male	0.000	0.000	0.000
Female (β_1)	0.477 (0.035)	0.498 (0.037)	0.454 (0.049)
Father Soc. Class 1980			
Employers etc	0.000	0.000	0.000
Non-manual (β_2)	-0.110 (0.068)	-0.104 (0.073)	-0.177 (0.092)
Manual (β_3)	0.165 (0.064)	0.166 (0.069)	0.134 (0.087)
Unclassifiable (β_4)	0.580 (0.068)	0.559 (0.073)	0.484 (0.093)
Hhold Income Quintile			
Quintile 1	0.000	0.000	0.000
Quintile 2 (β_5)	-0.133 (0.052)	-0.144 (0.056)	-0.236 (0.073)
Quintile 3 (β_6)	-0.166 (0.054)	-0.165 (0.057)	-0.271 (0.076)
Quintile 4 (β_7)	-0.094 (0.056)	-0.097 (0.060)	-0.231 (0.080)
Quintile 5 (β_8)	-0.249 (0.064)	-0.286 (0.068)	-0.402 (0.087)
Missing (β_9)	0.491 (0.068)	0.465 (0.072)	0.397 (0.095)
Housing Tenure			
Owner Occupied	0.000	0.000	0.000
Rented (β_{10})	0.471 (0.037)	0.480 (0.039)	0.449 (0.051)
Birth Cohort			
1972	0.000	0.000	0.000
1977 (β_{11})	-0.024 (0.035)	-0.037 (0.037)	-0.514 (0.156)
Economic Region			
Metropolitan		0.000	0.000
Larger Regional (β_{12})		-0.074 (0.043)	-0.100 (0.056)
Smaller Regional (β_{13})		-0.115 (0.061)	-0.271 (0.083)
Private Enterprise(β_{14})		0.147 (0.099)	0.188 (0.123)
Public Sector (β_{15})		-0.032 (0.133)	-0.219 (0.187)

Cohort*Sex			
1972*Male			0.000
1977*Female (β_{16})			0.102 (0.074)
Cohort*Soc. Class			
1972*Employers etc			0.000
1977*Non-manual (β_{17})			0.166 (0.152)
1977*Manual (β_{18})			0.080 (0.142)
1977*Unclass. (β_{19})			0.180 (0.151)
Cohort*Income			
1972*Quintile 1			0.000
1977*Quintile 2 (β_{20})			0.210 (0.113)
1977*Quintile 3 (β_{21})			0.242 (0.116)
1977*Quintile 4 (β_{22})			0.301 (0.120)
1977*Quintile 5 (β_{23})			0.277 (0.139)
1977*Missing (β_{24})			0.151 (0.145)
Cohort*Housing Tenure			
1972*Owner Occupied			0.000
1977*Rented (β_{25})			0.080 (0.079)
Cohort*Region			
1972*Metropolitan			0.000*
1977*Larger reg. (β_{26})			0.064 (0.083)
1977*Smaller reg. (β_{27})			0.344 (0.118)
1977*Private (β_{28})			-0.108 (0.197)
1977*Public (β_{29})			0.417 (0.260)
Random			
Parish Variation(σ_u^2)	0.022 (0.011)	0.017 (0.011)	0.017 (0.011)
Municipal. Variation(σ_v^2)	0.000 (0.000)	0.000 (0.000)	0.000 (0.000)

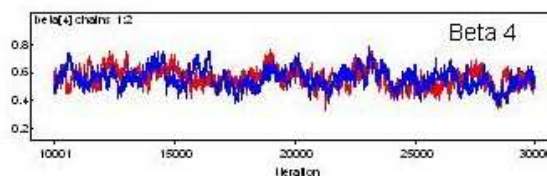
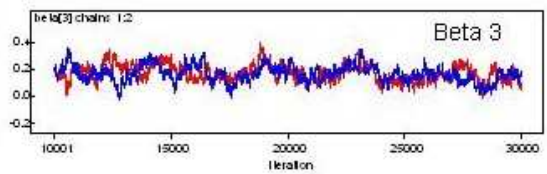
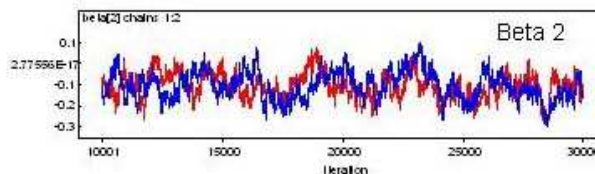
Appendix 8: Trace Plots and Gelman-Rubin Plots from Swedish Weibull Model

When fitting the Weibull ‘Individual+Area’ model with all significant covariates to the Swedish dataset, Section 9.4.4 only displayed trace plots and Gelman-Rubin plots for the intercept, ‘cohort’ regression parameter, shape parameter and random effects variance. Trace plots and Gelman-Rubin plots for the other regression parameters in the model are given below.

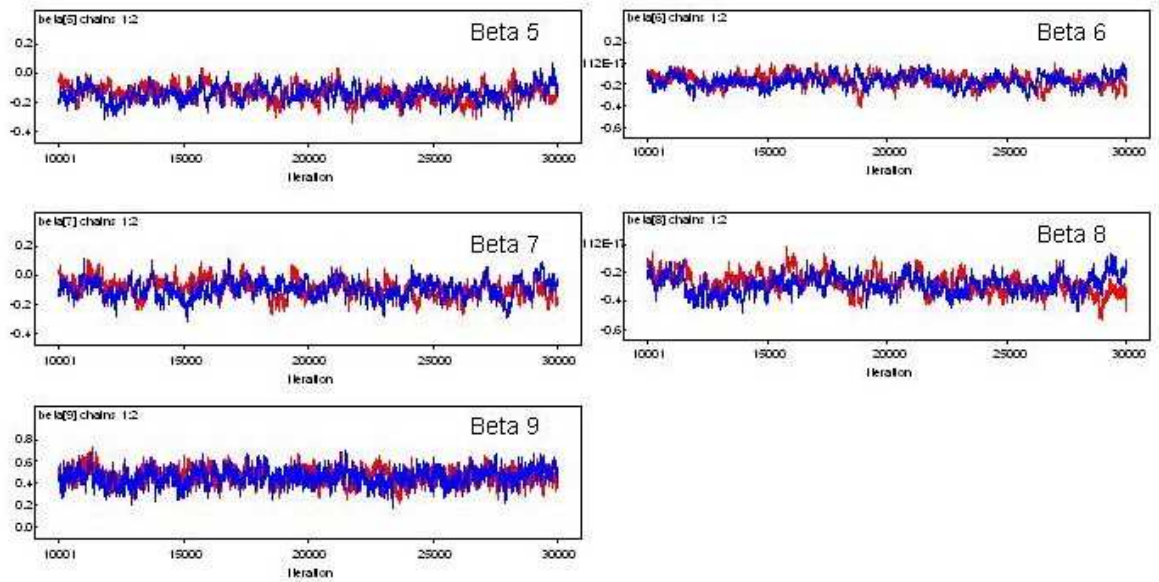
Trace Plots



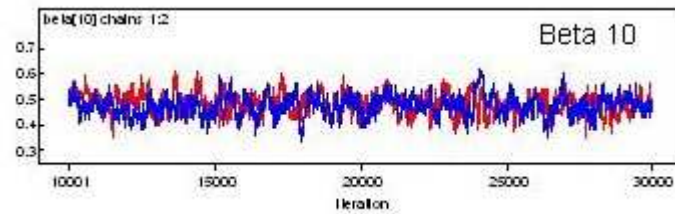
Sex



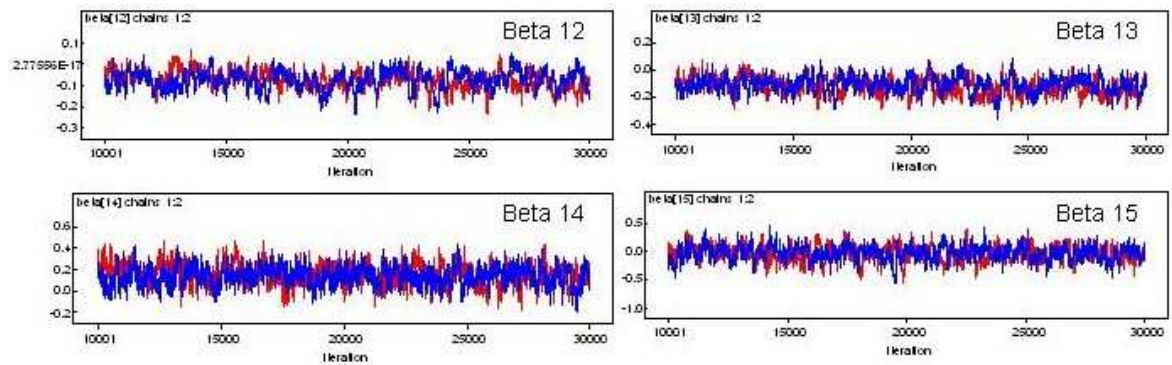
Father's Social Class in 1980



Household Income Quintile at Birth

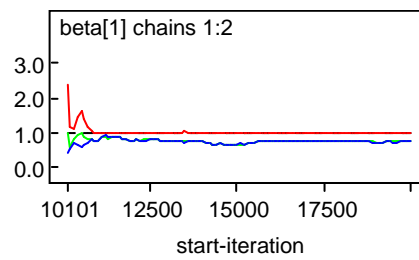


Housing Tenure at Birth

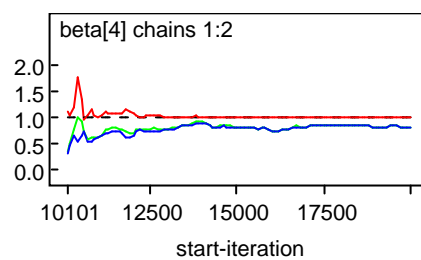
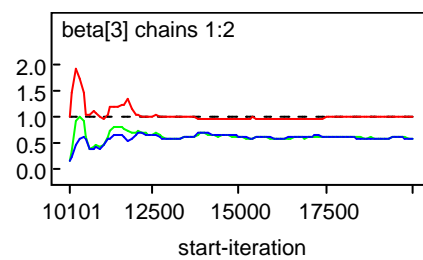
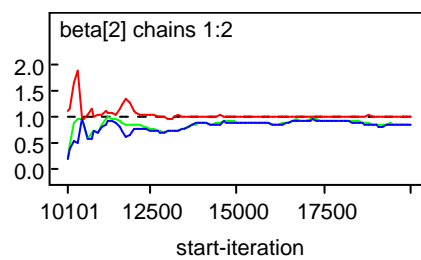


Economic Region

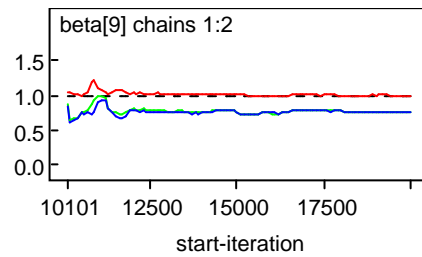
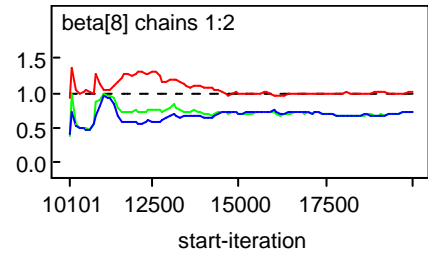
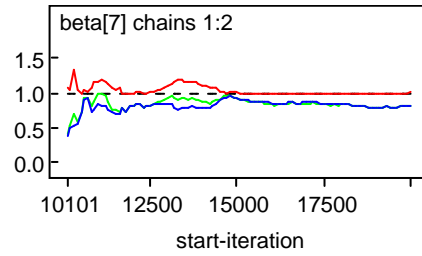
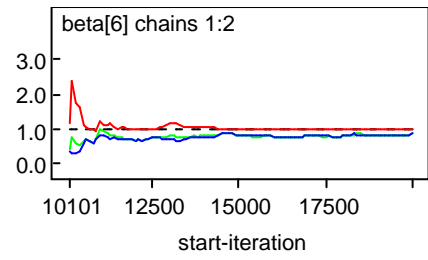
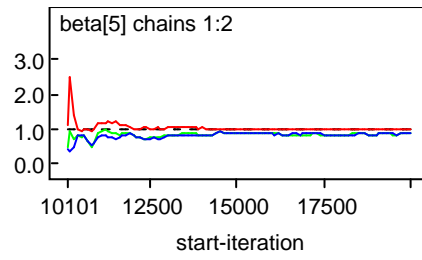
Gelman-Rubin Plots



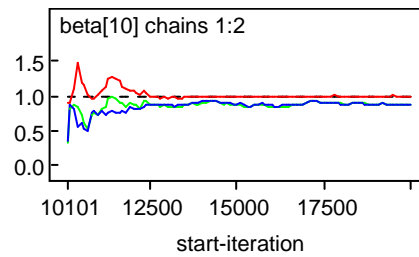
Sex



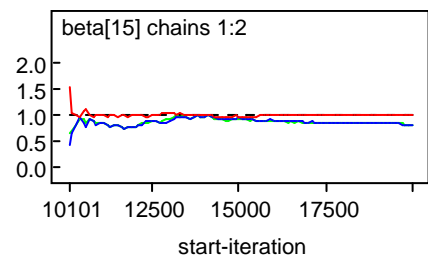
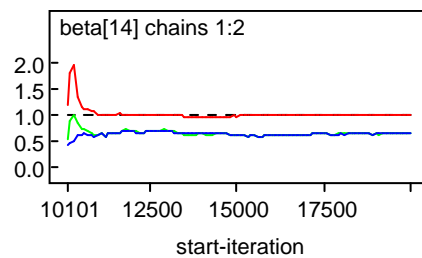
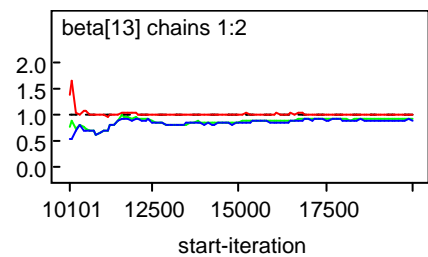
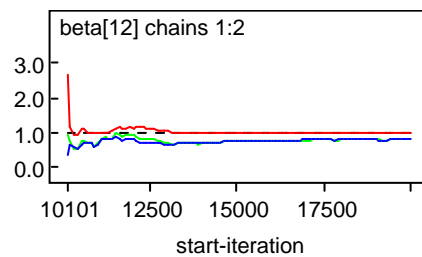
Father's Social Class in 1980



Household Income at Birth



Housing Tenure at Birth



Economic Region

Appendix 9: WinBUGS code for the Weibull Model with Different Shape Parameters

The WinBUGS code for the Weibull model with shape parameter defined separately for each cohort is given below.

```
model
{
  for (i in 1:N) {
    time[i] ~ dweib(r[cohort_77[i]+1],mu[i]) I(censor[i],)
    log(mu[i]) <- alpha + beta[1] * Female[i]
    + beta[2] * Non_manual_workers[i]
    + beta[3] * Manual_workers[i]
    + beta[4] * Unclassifiable_and_missing[i]
    + beta[5] * hh_incbth_2[i]
    + beta[6] * hh_incbth_3[i]
    + beta[7] * hh_incbth_4[i]
    + beta[8] * hh_incbth_5[i]
    + beta[9] * hh_incbth_miss[i]
    + beta[10] * rented[i]
    + beta[11] * cohort_77[i]
    + beta[12] * Larger_regional_centres[i]
    + beta[13] * Smaller_regional_centres[i]
    + beta[14] * Small_regions____mostly_private_enterprises[i]
    + beta[15] * Small_regions____mostly_public_sector[i]
    + u2[parbth[i]]
  }
  for (j in 1:n2){
    u2[j] ~ dnorm(0.0, tau.u2)
  }
  # Priors:
  alpha ~ dnorm(0.0, 0.0001)
  for (k in 1:15){
    beta[k] ~ dnorm(0.0, 0.0001)
  }
  logr[1] ~ dnorm(0, 0.1)
  logr[2] ~ dnorm(0, 0.1)
  r[1] <-exp(logr[1])
  r[2] <-exp(logr[2])
  # Priors for random effects variance
  sigma.u2~ dunif(0,3)
  sigma2.u2 <- sigma.u2*sigma.u2
  tau.u2<-1/sigma2.u2
}
```


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